

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 19:30:11 ; Search time 946.5 Seconds
(without alignments)
1981.864 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
c 1	33	100.0	33	6	AR447267	AR447267 Sequence	
2	33	100.0	33	6	AR447269	AR447269 Sequence	

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 18:00:00 ; Search time 224 Seconds
 (without alignments)
 981.852 Million cell updates/sec

Title: US-10-662-003-3
 Perfect score: 33
 Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_21:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		ID	Description
	No.	Score	Match	Length	DB			
c	1	33	100.0	33	2	AAX61005	Aax61005	Myostatin
	2	33	100.0	33	2	AAX61007	Aax61007	Myostatin

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 19:53:11 ; Search time 74 Seconds
(without alignments)
792.696 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGT TTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 20:01:25 ; Search time 406 Seconds
(without alignments)
672.142 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	33	100.0	33	7	US-10-662-003-1	Sequence 1, Appli
	2	33	100.0	33	7	US-10-662-003-3	Sequence 3, Appli

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 20:08:42 ; Search time 161 Seconds
(without alignments)
107.451 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4172979 seqs, 262114271 residues

Word size : 33

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 19:33:31 ; Search time 1872 Seconds
(without alignments)
824.772 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 33

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 14:29:03 ; Search time 1103.62 Seconds
(without alignments)
1699.710 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
<hr/>							
c	1	33	100.0	33	6	AR447267	AR447267 Sequence
	2	33	100.0	33	6	AR447269	AR447269 Sequence
	3	24	72.7	494	4	AH013313S3	AY254098 Bubalus b
	4	24	72.7	1599	4	AY787760S2	AY787761 Bos grunn
	5	24	72.7	5101	4	DQ091762	DQ091762 Bubalus b
	6	24	72.7	5790	6	BD080061	BD080061 Mutation

	7	24	72.7	6619	4	AY850105	AY850105 Bos tauru
	8	24	72.7	6660	4	AB076403	AB076403 Bos tauru
	9	24	72.7	6686	4	AY794986	AY794986 Bos indic
	10	24	72.7	6691	4	AF320998	AF320998 Bos tauru
c	11	24	72.7	192431	14	AC141853	AC141853 Bos tauru
c	12	24	72.7	233029	14	AC141852	AC141852 Bos tauru
	13	22	66.7	481	4	AY854495S3	AY854497 Bubalus b
	14	22	66.7	242679	14	AC117867	AC117867 Rattus no
	15	19	57.6	7331	6	AX347086	AX347086 Sequence
c	16	18	54.5	3255	15	AK110029	AK110029 Oryza sat
	17	18	54.5	136105	8	AC023508	AC023508 Homo sapi
	18	18	54.5	161754	9	AL662806	AL662806 Mouse DNA
c	19	18	54.5	170517	14	AC069526	AC069526 Homo sapi
	20	18	54.5	188660	5	CR753838	CR753838 Zebrafish
c	21	17	51.5	603	10	BV246247	BV246247 S234P6423
	22	17	51.5	897	9	AF162890S3	AF162892 Mus muscu
c	23	17	51.5	4809	6	AR278595	AR278595 Sequence
c	24	17	51.5	4809	6	AR400327	AR400327 Sequence
c	25	17	51.5	4809	6	AR405594	AR405594 Sequence
c	26	17	51.5	4809	6	AR563974	AR563974 Sequence
c	27	17	51.5	4809	6	AR588960	AR588960 Sequence
c	28	17	51.5	4809	6	AR605780	AR605780 Sequence
c	29	17	51.5	4809	6	AR657119	AR657119 Sequence
c	30	17	51.5	4809	6	AX200939	AX200939 Sequence
c	31	17	51.5	4809	6	AX267595	AX267595 Sequence
c	32	17	51.5	48086	8	HS1041B16	AL031223 Human DNA
	33	17	51.5	53985	8	AL357121	AL357121 Human DNA
	34	17	51.5	72273	14	AC090859	AC090859 Homo sapi
	35	17	51.5	77875	14	AC165750	AC165750 Bos tauru
	36	17	51.5	96262	5	CR388129	CR388129 Zebrafish
	37	17	51.5	110000	14	CT009752_3	Continuation (4 of
	38	17	51.5	110000	14	CT009753_06	Continuation (7 of
c	39	17	51.5	143420	8	AL161422	AL161422 Human DNA
	40	17	51.5	152414	9	AC129553	AC129553 Mus muscu
c	41	17	51.5	156367	9	AC126034	AC126034 Mus muscu
	42	17	51.5	162044	8	AL159980	AL159980 Human DNA
c	43	17	51.5	162628	9	AC153932	AC153932 Mus muscu
c	44	17	51.5	168606	8	AC147274	AC147274 Pan trogl
c	45	17	51.5	173683	9	AC153979	AC153979 Mus muscu

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 14:23:33 ; Search time 265.671 Seconds
(without alignments)
827.847 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGT TTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			% Query		DB	ID	Description
	No.	Score	Match	Length			
c	1	33	100.0	33	2	AAX61005	Aax61005 Myostatin
	2	33	100.0	33	2	AAX61007	Aax61007 Myostatin
	3	24	72.7	5790	2	AAX24464	Aax24464 Bovine my
	4	19	57.6	7331	6	ABL34184	Abl34184 Human imm
c	5	17	51.5	4809	4	AAH93831	Aah93831 Human pro
c	6	17	51.5	4809	4	AAS63924	Aas63924 Human pro
c	7	17	51.5	4809	5	ACA59732	Aca59732 Prostate

c	8	17	51.5	4809	6	ABL95295	Abl95295 Human P77
c	9	17	51.5	4809	8	ACC95459	Acc95459 Prostate
c	10	17	51.5	4809	10	ADB14019	Adb14019 Human pro
c	11	17	51.5	4809	10	ADG26435	Adg26435 Human pro
	12	16	48.5	457	10	ADB51306	Adb51306 Primary r
	13	16	48.5	582	6	ABQ36544	Abq36544 Oligonucl
c	14	16	48.5	582	6	ABQ36545	Abq36545 Oligonucl
c	15	16	48.5	1231	5	AAC88115	Aac88115 Human FLE
	16	16	48.5	1396	3	AAC39628	Aac39628 Arabidops
c	17	16	48.5	6992	13	ADR84211	Adr84211 Aspergill
	18	16	48.5	15518	6	ABL34173	Abl34173 Human imm
	19	16	48.5	15518	6	ABL34625	Abl34625 Human met
	20	16	48.5	15518	6	ABL70608	Abl70608 Chemicall
	21	16	48.5	15518	7	ADS99886	Ads99886 Complemen
c	22	16	48.5	41239	4	AAK78622	Aak78622 Human imm
	23	16	48.5	61020	4	AAS46787	Aas46787 Tumour su
	24	16	48.5	201239	8	ACA64924	Aca64924 Human PLZ
	25	15	45.5	24	14	AEA54359	Aea54359 Primer fo
	26	15	45.5	137	4	AAI19807	Aai19807 Probe #97
	27	15	45.5	137	4	ABA64834	Aba64834 Human foe
	28	15	45.5	137	4	AAI45002	Aai45002 Probe #13
	29	15	45.5	137	4	ABA46953	Aba46953 Human bre
	30	15	45.5	137	4	ABA31950	Aba31950 Probe #10
	31	15	45.5	137	4	AAK38997	Aak38997 Human bon
	32	15	45.5	137	4	AAK13263	Aak13263 Human bra
	33	15	45.5	137	4	ABS38584	Abs38584 Human liv
	34	15	45.5	137	5	AAI05523	Aai05523 Probe #55
	35	15	45.5	137	6	ABS13081	Abs13081 Human gen
c	36	15	45.5	379	9	ACH50331	Ach50331 Human leu
c	37	15	45.5	481	4	AAI10548	Aai10548 Probe #48
c	38	15	45.5	481	4	ABA52195	Aba52195 Human foe
c	39	15	45.5	481	4	AAI31801	Aai31801 Probe #48
c	40	15	45.5	481	4	ABA22000	Aba22000 Probe #46
c	41	15	45.5	481	4	AAK25918	Aak25918 Human bon
c	42	15	45.5	481	4	AAK00471	Aak00471 Human bra
c	43	15	45.5	481	4	ABS25507	Abs25507 Human liv
c	44	15	45.5	481	5	AAI00480	Aai00480 Probe #47
c	45	15	45.5	481	6	ABS00501	Abs00501 Human gen

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:54:27 ; Search time 82.2911 Seconds
 (without alignments)
 712.829 Million cell updates/sec

Title: US-10-662-003-3
 Perfect score: 33
 Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGT TTTGGGATC 33

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	33	100.0	33	3	US-08-967-089A-1	Sequence 1, Appli
	2	33	100.0	33	3	US-08-967-089A-3	Sequence 3, Appli
c	3	17	51.5	4809	3	US-09-636-215-569	Sequence 569, App
c	4	17	51.5	4809	3	US-09-685-166A-569	Sequence 569, App
c	5	17	51.5	4809	3	US-09-679-426-569	Sequence 569, App
c	6	17	51.5	4809	3	US-09-759-143-569	Sequence 569, App
c	7	17	51.5	4809	3	US-09-651-236-569	Sequence 569, App
c	8	17	51.5	4809	3	US-09-657-279-569	Sequence 569, App
c	9	17	51.5	4809	3	US-10-012-896-569	Sequence 569, App
	10	16	48.5	191433	3	US-09-949-016-16144	Sequence 16144, A
c	11	15	45.5	18895	3	US-09-949-016-14698	Sequence 14698, A
c	12	15	45.5	113100	3	US-09-949-016-12245	Sequence 12245, A

c	13	15	45.5	246444	3	US-09-949-016-13113	Sequence 13113, A
c	14	15	45.5	360470	3	US-09-949-016-13173	Sequence 13173, A
	15	14	42.4	36	2	US-09-066-074-4	Sequence 4, Appli
	16	14	42.4	36	2	US-08-555-912A-4	Sequence 4, Appli
	17	14	42.4	36	3	US-09-275-900-4	Sequence 4, Appli
	18	14	42.4	172	3	US-09-513-999C-16176	Sequence 16176, A
c	19	14	42.4	340	3	US-09-270-767-29318	Sequence 29318, A
c	20	14	42.4	475	3	US-09-621-976-14039	Sequence 14039, A
	21	14	42.4	601	3	US-09-949-016-17909	Sequence 17909, A
	22	14	42.4	601	3	US-09-949-016-20187	Sequence 20187, A
	23	14	42.4	601	3	US-09-949-016-31821	Sequence 31821, A
	24	14	42.4	601	3	US-09-949-016-40006	Sequence 40006, A
	25	14	42.4	601	3	US-09-949-016-41799	Sequence 41799, A
c	26	14	42.4	601	3	US-09-949-016-53060	Sequence 53060, A
	27	14	42.4	601	3	US-09-949-016-73967	Sequence 73967, A
	28	14	42.4	601	3	US-09-949-016-74073	Sequence 74073, A
c	29	14	42.4	601	3	US-09-949-016-103306	Sequence 103306,
c	30	14	42.4	601	3	US-09-949-016-115136	Sequence 115136,
	31	14	42.4	601	3	US-09-949-016-163364	Sequence 163364,
	32	14	42.4	601	3	US-09-949-016-165433	Sequence 165433,
	33	14	42.4	601	3	US-09-949-016-165490	Sequence 165490,
	34	14	42.4	785	3	US-09-270-767-9468	Sequence 9468, Ap
	35	14	42.4	785	3	US-09-270-767-24750	Sequence 24750, A
c	36	14	42.4	1001	3	US-09-671-317-51	Sequence 51, Appl
	37	14	42.4	1086	3	US-09-807-784B-4	Sequence 4, Appli
c	38	14	42.4	1111	3	US-09-949-016-4873	Sequence 4873, Ap
	39	14	42.4	1268	3	US-09-574-942-3	Sequence 3, Appli
	40	14	42.4	1268	3	US-09-949-434-3	Sequence 3, Appli
	41	14	42.4	1268	3	US-10-240-709-3	Sequence 3, Appli
c	42	14	42.4	1281	3	US-09-976-594-944	Sequence 944, App
c	43	14	42.4	1435	3	US-09-620-312D-373	Sequence 373, App
c	44	14	42.4	1449	3	US-09-270-767-13364	Sequence 13364, A
	45	14	42.4	1956	3	US-09-134-000C-1450	Sequence 1450, Ap

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:05:38 ; Search time 489.152 Seconds
(without alignments)
557.883 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGT TTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		Length	DB	ID	Description
			Match					
c	1	33	100.0		33	7	US-10-662-003-1	Sequence 1, Appli
	2	33	100.0		33	7	US-10-662-003-3	Sequence 3, Appli
	3	24	72.7		5790	6	US-10-251-115-54	Sequence 54, Appl
	4	19	57.6		7331	6	US-10-311-455-2157	Sequence 2157, Ap
c	5	17	51.5		635	5	US-10-027-632-227137	Sequence 227137,
c	6	17	51.5		635	6	US-10-027-632-227137	Sequence 227137,
c	7	17	51.5		4809	3	US-09-759-143-569	Sequence 569, App
c	8	17	51.5		4809	3	US-09-780-669-569	Sequence 569, App
c	9	17	51.5		4809	3	US-09-822-827-569	Sequence 569, App
c	10	17	51.5		4809	3	US-09-895-793-569	Sequence 569, App
c	11	17	51.5		4809	3	US-09-895-814-569	Sequence 569, App

c	12	17	51.5	4809	5	US-10-012-896-569	Sequence 569, App
c	13	17	51.5	4809	6	US-10-144-678A-569	Sequence 569, App
c	14	17	51.5	4809	6	US-10-294-025-569	Sequence 569, App
c	15	16	48.5	25	7	US-10-719-956-58863	Sequence 58863, A
	16	16	48.5	332	4	US-09-925-065A-447267	Sequence 447267,
	17	16	48.5	531	4	US-09-925-065A-315605	Sequence 315605,
	18	16	48.5	582	8	US-10-363-345A-23135	Sequence 23135, A
c	19	16	48.5	582	8	US-10-363-345A-23136	Sequence 23136, A
	20	16	48.5	582	9	US-10-363-483A-23135	Sequence 23135, A
c	21	16	48.5	582	9	US-10-363-483A-23136	Sequence 23136, A
	22	16	48.5	597	4	US-09-925-065A-447266	Sequence 447266,
	23	16	48.5	599	9	US-10-972-079-78646	Sequence 78646, A
	24	16	48.5	599	9	US-10-972-079-78647	Sequence 78647, A
	25	16	48.5	600	9	US-10-972-079-38327	Sequence 38327, A
	26	16	48.5	600	9	US-10-972-079-38328	Sequence 38328, A
	27	16	48.5	600	9	US-10-972-079-78648	Sequence 78648, A
c	28	16	48.5	604	4	US-09-925-065A-540809	Sequence 540809,
	29	16	48.5	604	5	US-10-027-632-89762	Sequence 89762, A
	30	16	48.5	604	6	US-10-027-632-89762	Sequence 89762, A
	31	16	48.5	15518	6	US-10-311-455-2146	Sequence 2146, Ap
	32	16	48.5	15518	6	US-10-240-485-178	Sequence 178, App
	33	16	48.5	61020	7	US-10-221-714A-513	Sequence 513, App
	34	16	48.5	201239	8	US-10-278-698-246	Sequence 246, App
	35	16	48.5	201239	8	US-10-278-698-760	Sequence 760, App
c	36	16	48.5	394468	8	US-10-741-600-17952	Sequence 17952, A
c	37	15	45.5	25	7	US-10-719-956-655177	Sequence 655177,
	38	15	45.5	137	3	US-09-864-761-17270	Sequence 17270, A
	39	15	45.5	149	8	US-10-425-115-147155	Sequence 147155,
	40	15	45.5	201	8	US-10-741-600-45861	Sequence 45861, A
	41	15	45.5	256	8	US-10-425-115-130956	Sequence 130956,
c	42	15	45.5	379	3	US-09-918-995-37543	Sequence 37543, A
c	43	15	45.5	391	7	US-10-437-963-84414	Sequence 84414, A
	44	15	45.5	419	5	US-10-027-632-183556	Sequence 183556,
	45	15	45.5	419	5	US-10-027-632-183557	Sequence 183557,

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:15:55 ; Search time 198 Seconds
 (without alignments)
 87.371 Million cell updates/sec

Title: US-10-662-003-3
 Perfect score: 33
 Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 4172979 seqs, 262114271 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
c	1	16	48.5	394468	6	US-10-995-561-13473	Sequence 13473, A
	2	15	45.5	160226	7	US-11-121-086-29	Sequence 29, Appl
	3	15	45.5	172111	7	US-11-121-086-28	Sequence 28, Appl
c	4	15	45.5	218821	7	US-11-121-086-31	Sequence 31, Appl
	5	14	42.4	201	6	US-10-995-561-65754	Sequence 65754, A
	6	14	42.4	1364	6	US-10-750-185-29566	Sequence 29566, A
c	7	14	42.4	1474	6	US-10-750-185-60465	Sequence 60465, A
c	8	14	42.4	1488	6	US-10-750-185-36129	Sequence 36129, A
c	9	14	42.4	1787	6	US-10-750-185-61408	Sequence 61408, A
c	10	14	42.4	1790	6	US-10-750-185-28338	Sequence 28338, A
	11	14	42.4	1929	6	US-10-750-185-43244	Sequence 43244, A

c	12	14	42.4	3480	6	US-10-750-185-30715	Sequence 30715, A
c	13	14	42.4	14670	6	US-10-995-561-13328	Sequence 13328, A
	14	14	42.4	42419	6	US-10-995-561-13205	Sequence 13205, A
	15	14	42.4	48203	6	US-10-995-561-13378	Sequence 13378, A
c	16	14	42.4	180654	7	US-11-121-086-58	Sequence 58, Appl
	17	14	42.4	182190	7	US-11-121-086-102	Sequence 102, App
	18	14	42.4	246960	7	US-11-121-086-8	Sequence 8, Appli
	19	14	42.4	387780	6	US-10-995-561-13259	Sequence 13259, A
	20	14	42.4	1080000	6	US-10-928-446A-1	Sequence 1, Appli
c	21	14	42.4	1080000	6	US-10-928-446A-1	Sequence 1, Appli
	22	14	42.4	1080000	6	US-10-928-446A-181	Sequence 181, App
c	23	14	42.4	1080000	6	US-10-928-446A-181	Sequence 181, App
	24	14	42.4	1080000	6	US-10-928-446A-183	Sequence 183, App
c	25	14	42.4	1080000	6	US-10-928-446A-183	Sequence 183, App
	26	14	42.4	1080000	6	US-10-928-446A-185	Sequence 185, App
c	27	14	42.4	1080000	6	US-10-928-446A-185	Sequence 185, App
	28	14	42.4	1080000	6	US-10-928-446A-187	Sequence 187, App
c	29	14	42.4	1080000	6	US-10-928-446A-187	Sequence 187, App
	30	14	42.4	1080000	6	US-10-928-446A-189	Sequence 189, App
c	31	14	42.4	1080000	6	US-10-928-446A-189	Sequence 189, App
	32	14	42.4	1080000	6	US-10-928-446A-191	Sequence 191, App
c	33	14	42.4	1080000	6	US-10-928-446A-191	Sequence 191, App
	34	14	42.4	1080000	6	US-10-928-446A-193	Sequence 193, App
c	35	14	42.4	1080000	6	US-10-928-446A-193	Sequence 193, App
	36	14	42.4	1080000	6	US-10-928-446A-195	Sequence 195, App
c	37	14	42.4	1080000	6	US-10-928-446A-195	Sequence 195, App
	38	14	42.4	1080000	6	US-10-928-446A-197	Sequence 197, App
c	39	14	42.4	1080000	6	US-10-928-446A-197	Sequence 197, App
	40	14	42.4	1080000	6	US-10-928-446A-199	Sequence 199, App
c	41	14	42.4	1080000	6	US-10-928-446A-199	Sequence 199, App
	42	14	42.4	1080000	6	US-10-928-446A-201	Sequence 201, App
c	43	14	42.4	1080000	6	US-10-928-446A-201	Sequence 201, App
c	44	13	39.4	19	8	US-11-101-244-35439	Sequence 35439, A
c	45	13	39.4	19	8	US-11-101-244-755073	Sequence 755073,

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:29:54 ; Search time 2256.11 Seconds
 (without alignments)
 684.351 Million cell updates/sec

Title: US-10-662-003-3
 Perfect score: 33
 Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_est3:*
 4: gb_htc:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_est7:*
 9: gb_gss1:*
 10: gb_gss2:*
 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Match	Length	DB	ID	
c	1	24	72.7	797	9	CC562316	CC562316 CH240_473
	2	19	57.6	193	2	BB596484	BB596484 BB596484
c	3	18	54.5	987	2	BF348308	BF348308 602022330
	4	18	54.5	996	10	DU019690	DU019690 276171 To
c	5	17	51.5	342	6	CB471707	CB471707 sn43_D10.
c	6	17	51.5	405	6	CB811102	CB811102 AMGNNUC:S
c	7	17	51.5	407	6	CB240457	CB240457 PopSC0044
c	8	17	51.5	418	9	AQ944443	AQ944443 Sheared D
c	9	17	51.5	513	3	BI317706	BI317706 saf26b05.
c	10	17	51.5	546	6	CA823772	CA823772 R31B05 tw

c	11	17	51.5	569	1	AI597805	AI597805	tu91f01.x
c	12	17	51.5	584	2	BG046547	BG046547	saa55g09.
c	13	17	51.5	592	5	BU893013	BU893013	P072B12 P
c	14	17	51.5	600	9	AZ287062	AZ287062	RPCI-23-1
c	15	17	51.5	602	6	CF755762	CF755762	DSAF1_1_E
c	16	17	51.5	649	6	CA821419	CA821419	RSH02F07
c	17	17	51.5	682	6	CF233748	CF233748	PtaJX0002
	18	17	51.5	698	8	CV784168	CV784168	UI-M-HY0p
c	19	17	51.5	704	6	CF235883	CF235883	PtaJXT002
c	20	17	51.5	709	9	AQ924237	AQ924237	RPCI-23-2
c	21	17	51.5	712	11	CR325351	CR325351	mtel-52J8
	22	17	51.5	720	5	BW387967	BW387967	BW387967
c	23	17	51.5	731	10	CW491521	CW491521	fsbb001f2
c	24	17	51.5	747	6	CA784231	CA784231	sat95h11.
c	25	17	51.5	772	6	CF236754	CF236754	PtaJXT6G4
c	26	17	51.5	887	10	CL072223	CL072223	CH216-123
c	27	17	51.5	889	10	CNS0208U	AL175287	Tetraodon
	28	17	51.5	1055	10	AG428671	AG428671	Mus muscu
	29	16	48.5	197	10	CZ905322	CZ905322	Barr-ASLV
c	30	16	48.5	290	9	CC369758	CC369758	PUHGA90TD
c	31	16	48.5	360	7	CN486449	CN486449	EST1095 P
	32	16	48.5	389	9	CC417010	CC417010	PUHMA94TD
c	33	16	48.5	433	9	AQ812568	AQ812568	HS_5249_B
c	34	16	48.5	443	5	BQ988981	BQ988981	QGF16G19.
	35	16	48.5	447	1	AW930709	AW930709	EST356552
	36	16	48.5	456	2	BF386560	BF386560	UI-R-CA1-
	37	16	48.5	457	1	AI101818	AI101818	EST211107
	38	16	48.5	460	1	AA901148	AA901148	UI-R-A1-d
	39	16	48.5	474	2	BF393516	BF393516	UI-R-CA0-
c	40	16	48.5	479	9	CC417007	CC417007	PUHMA94TB
c	41	16	48.5	484	6	CB252858	CB252858	16-E01404
c	42	16	48.5	491	1	AU084800	AU084800	AU084800
	43	16	48.5	500	2	BF392300	BF392300	UI-R-CA0-
c	44	16	48.5	500	6	CD583691	CD583691	RK021A1E0
	45	16	48.5	505	9	BZ310915	BZ310915	ic60h12.b

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:54:27 ; Search time 82.2911 Seconds
(without alignments)
712.829 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
c	1	33	100.0	33	3	US-08-967-089A-1	Sequence 1, Appli
	2	33	100.0	33	3	US-08-967-089A-3	Sequence 3, Appli
c	3	17	51.5	4809	3	US-09-636-215-569	Sequence 569, App
c	4	17	51.5	4809	3	US-09-685-166A-569	Sequence 569, App
c	5	17	51.5	4809	3	US-09-679-426-569	Sequence 569, App
c	6	17	51.5	4809	3	US-09-759-143-569	Sequence 569, App
c	7	17	51.5	4809	3	US-09-651-236-569	Sequence 569, App
c	8	17	51.5	4809	3	US-09-657-279-569	Sequence 569, App
c	9	17	51.5	4809	3	US-10-012-896-569	Sequence 569, App
	10	16	48.5	191433	3	US-09-949-016-16144	Sequence 16144, A
c	11	15	45.5	18895	3	US-09-949-016-14698	Sequence 14698, A
c	12	15	45.5	113100	3	US-09-949-016-12245	Sequence 12245, A

c	13	15	45.5	246444	3	US-09-949-016-13113	Sequence 13113, A
c	14	15	45.5	360470	3	US-09-949-016-13173	Sequence 13173, A
	15	14	42.4	36	2	US-09-066-074-4	Sequence 4, Appli
	16	14	42.4	36	2	US-08-555-912A-4	Sequence 4, Appli
	17	14	42.4	36	3	US-09-275-900-4	Sequence 4, Appli
	18	14	42.4	172	3	US-09-513-999C-16176	Sequence 16176, A
c	19	14	42.4	340	3	US-09-270-767-29318	Sequence 29318, A
c	20	14	42.4	475	3	US-09-621-976-14039	Sequence 14039, A
	21	14	42.4	601	3	US-09-949-016-17909	Sequence 17909, A
	22	14	42.4	601	3	US-09-949-016-20187	Sequence 20187, A
	23	14	42.4	601	3	US-09-949-016-31821	Sequence 31821, A
	24	14	42.4	601	3	US-09-949-016-40006	Sequence 40006, A
	25	14	42.4	601	3	US-09-949-016-41799	Sequence 41799, A
c	26	14	42.4	601	3	US-09-949-016-53060	Sequence 53060, A
	27	14	42.4	601	3	US-09-949-016-73967	Sequence 73967, A
	28	14	42.4	601	3	US-09-949-016-74073	Sequence 74073, A
c	29	14	42.4	601	3	US-09-949-016-103306	Sequence 103306,
c	30	14	42.4	601	3	US-09-949-016-115136	Sequence 115136,
	31	14	42.4	601	3	US-09-949-016-163364	Sequence 163364,
	32	14	42.4	601	3	US-09-949-016-165433	Sequence 165433,
	33	14	42.4	601	3	US-09-949-016-165490	Sequence 165490,
	34	14	42.4	785	3	US-09-270-767-9468	Sequence 9468, Ap
	35	14	42.4	785	3	US-09-270-767-24750	Sequence 24750, A
c	36	14	42.4	1001	3	US-09-671-317-51	Sequence 51, Appl
	37	14	42.4	1086	3	US-09-807-784B-4	Sequence 4, Appli
c	38	14	42.4	1111	3	US-09-949-016-4873	Sequence 4873, Ap
	39	14	42.4	1268	3	US-09-574-942-3	Sequence 3, Appli
	40	14	42.4	1268	3	US-09-949-434-3	Sequence 3, Appli
	41	14	42.4	1268	3	US-10-240-709-3	Sequence 3, Appli
c	42	14	42.4	1281	3	US-09-976-594-944	Sequence 944, App
c	43	14	42.4	1435	3	US-09-620-312D-373	Sequence 373, App
c	44	14	42.4	1449	3	US-09-270-767-13364	Sequence 13364, A
	45	14	42.4	1956	3	US-09-134-000C-1450	Sequence 1450, Ap

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:05:38 ; Search time 489.152 Seconds
(without alignments)
557.883 Million cell updates/sec

Title: US-10-662-003-3
Perfect score: 33
Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGT TTTGGGATC 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
c	1	33	100.0	33	7	US-10-662-003-1	Sequence 1, Appli
	2	33	100.0	33	7	US-10-662-003-3	Sequence 3, Appli
	3	24	72.7	5790	6	US-10-251-115-54	Sequence 54, Appl
	4	19	57.6	7331	6	US-10-311-455-2157	Sequence 2157, Ap
c	5	17	51.5	635	5	US-10-027-632-227137	Sequence 227137,
c	6	17	51.5	635	6	US-10-027-632-227137	Sequence 227137,
c	7	17	51.5	4809	3	US-09-759-143-569	Sequence 569, App
c	8	17	51.5	4809	3	US-09-780-669-569	Sequence 569, App
c	9	17	51.5	4809	3	US-09-822-827-569	Sequence 569, App
c	10	17	51.5	4809	3	US-09-895-793-569	Sequence 569, App
c	11	17	51.5	4809	3	US-09-895-814-569	Sequence 569, App

c	12	17	51.5	4809	5	US-10-012-896-569	Sequence 569, App
c	13	17	51.5	4809	6	US-10-144-678A-569	Sequence 569, App
c	14	17	51.5	4809	6	US-10-294-025-569	Sequence 569, App
c	15	16	48.5	25	7	US-10-719-956-58863	Sequence 58863, A
	16	16	48.5	332	4	US-09-925-065A-447267	Sequence 447267,
	17	16	48.5	531	4	US-09-925-065A-315605	Sequence 315605,
	18	16	48.5	582	8	US-10-363-345A-23135	Sequence 23135, A
c	19	16	48.5	582	8	US-10-363-345A-23136	Sequence 23136, A
	20	16	48.5	582	9	US-10-363-483A-23135	Sequence 23135, A
c	21	16	48.5	582	9	US-10-363-483A-23136	Sequence 23136, A
	22	16	48.5	597	4	US-09-925-065A-447266	Sequence 447266,
	23	16	48.5	599	9	US-10-972-079-78646	Sequence 78646, A
	24	16	48.5	599	9	US-10-972-079-78647	Sequence 78647, A
	25	16	48.5	600	9	US-10-972-079-38327	Sequence 38327, A
	26	16	48.5	600	9	US-10-972-079-38328	Sequence 38328, A
	27	16	48.5	600	9	US-10-972-079-78648	Sequence 78648, A
c	28	16	48.5	604	4	US-09-925-065A-540809	Sequence 540809,
	29	16	48.5	604	5	US-10-027-632-89762	Sequence 89762, A
	30	16	48.5	604	6	US-10-027-632-89762	Sequence 89762, A
	31	16	48.5	15518	6	US-10-311-455-2146	Sequence 2146, Ap
	32	16	48.5	15518	6	US-10-240-485-178	Sequence 178, App
	33	16	48.5	61020	7	US-10-221-714A-513	Sequence 513, App
	34	16	48.5	201239	8	US-10-278-698-246	Sequence 246, App
	35	16	48.5	201239	8	US-10-278-698-760	Sequence 760, App
c	36	16	48.5	394468	8	US-10-741-600-17952	Sequence 17952, A
c	37	15	45.5	25	7	US-10-719-956-655177	Sequence 655177,
	38	15	45.5	137	3	US-09-864-761-17270	Sequence 17270, A
	39	15	45.5	149	8	US-10-425-115-147155	Sequence 147155,
	40	15	45.5	201	8	US-10-741-600-45861	Sequence 45861, A
	41	15	45.5	256	8	US-10-425-115-130956	Sequence 130956,
c	42	15	45.5	379	3	US-09-918-995-37543	Sequence 37543, A
c	43	15	45.5	391	7	US-10-437-963-84414	Sequence 84414, A
	44	15	45.5	419	5	US-10-027-632-183556	Sequence 183556,
	45	15	45.5	419	5	US-10-027-632-183557	Sequence 183557,

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:29:54 ; Search time 2256.11 Seconds
 (without alignments)
 684.351 Million cell updates/sec

Title: US-10-662-003-3
 Perfect score: 33
 Sequence: 1 CGCGGATCCGAGGTAGGAGAGTGTTTTGGGATC 33

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_est3:*
 4: gb_htc:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_est7:*
 9: gb_gss1:*
 10: gb_gss2:*
 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
c	1	24	72.7	797	9	CC562316	CC562316 CH240_473
	2	19	57.6	193	2	BB596484	BB596484 BB596484
c	3	18	54.5	987	2	BF348308	BF348308 602022330
	4	18	54.5	996	10	DU019690	DU019690 276171 To
c	5	17	51.5	342	6	CB471707	CB471707 sn43_D10.
c	6	17	51.5	405	6	CB811102	CB811102 AMGNNUC:S
c	7	17	51.5	407	6	CB240457	CB240457 PopSC0044
c	8	17	51.5	418	9	AQ944443	AQ944443 Sheared D
c	9	17	51.5	513	3	BI317706	BI317706 saf26b05.
c	10	17	51.5	546	6	CA823772	CA823772 R31B05 tw

c	11	17	51.5	569	1	AI597805	AI597805	tu91f01.x
c	12	17	51.5	584	2	BG046547	BG046547	saa55g09.
c	13	17	51.5	592	5	BU893013	BU893013	P072B12 P
c	14	17	51.5	600	9	AZ287062	AZ287062	RPCI-23-1
c	15	17	51.5	602	6	CF755762	CF755762	DSAF1_1_E
c	16	17	51.5	649	6	CA821419	CA821419	RSH02F07
c	17	17	51.5	682	6	CF233748	CF233748	PtaJX0002
	18	17	51.5	698	8	CV784168	CV784168	UI-M-HY0p
c	19	17	51.5	704	6	CF235883	CF235883	PtaJXT002
c	20	17	51.5	709	9	AQ924237	AQ924237	RPCI-23-2
c	21	17	51.5	712	11	CR325351	CR325351	mtel-52J8
	22	17	51.5	720	5	BW387967	BW387967	BW387967
c	23	17	51.5	731	10	CW491521	CW491521	fsbb001f2
c	24	17	51.5	747	6	CA784231	CA784231	sat95h11.
c	25	17	51.5	772	6	CF236754	CF236754	PtaJXT6G4
c	26	17	51.5	887	10	CL072223	CL072223	CH216-123
c	27	17	51.5	889	10	CNS0208U	AL175287	Tetraodon
	28	17	51.5	1055	10	AG428671	AG428671	Mus muscu
	29	16	48.5	197	10	CZ905322	CZ905322	Barr-ASLV
c	30	16	48.5	290	9	CC369758	CC369758	PUHGA90TD
c	31	16	48.5	360	7	CN486449	CN486449	EST1095 P
	32	16	48.5	389	9	CC417010	CC417010	PUHMA94TD
c	33	16	48.5	433	9	AQ812568	AQ812568	HS_5249_B
c	34	16	48.5	443	5	BQ988981	BQ988981	QGF16G19.
	35	16	48.5	447	1	AW930709	AW930709	EST356552
	36	16	48.5	456	2	BF386560	BF386560	UI-R-CA1-
	37	16	48.5	457	1	AI101818	AI101818	EST211107
	38	16	48.5	460	1	AA901148	AA901148	UI-R-A1-d
	39	16	48.5	474	2	BF393516	BF393516	UI-R-CA0-
c	40	16	48.5	479	9	CC417007	CC417007	PUHMA94TB
c	41	16	48.5	484	6	CB252858	CB252858	16-E01404
c	42	16	48.5	491	1	AU084800	AU084800	AU084800
	43	16	48.5	500	2	BF392300	BF392300	UI-R-CA0-
c	44	16	48.5	500	6	CD583691	CD583691	RK021A1E0
	45	16	48.5	505	9	BZ310915	BZ310915	ic60h12.b

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 19:30:11 ; Search time 946.5 Seconds
(without alignments)
1981.864 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
c 1	33	100.0	33	6	AR447268	AR447268 Sequence	
2	33	100.0	33	6	AR447270	AR447270 Sequence	

ALIGNMENTS

```

AR447268/c
LOCUS       AR447268                33 bp    DNA        linear    PAT 20-FEB-2004
DEFINITION  Sequence 2 from patent US 6673534.
ACCESSION   AR447268
VERSION     AR447268.1   GI:42675563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1   (bases 1 to 33)
  AUTHORS   Lee,S.-J. and McPherron,A.C.
  TITLE     Methods for detection of mutations in myostatin variants
  JOURNAL   Patent: US 6673534-A 2 06-JAN-2004;
            The Johns Hopkins University School of Medicine; Baltimore, MD
FEATURES             Location/Qualifiers
     source             1..33
                       /organism="unknown"
                       /mol_type="genomic DNA"
ORIGIN

```

```
Query Match      100.0%;  Score 33;  DB 6;  Length 33;
Best Local Similarity 100.0%;  Pred. No. 9.4e-08;
Matches 33;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```

Qy      1 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 33
        ||||||||||||||||||||||||||||
Db     33 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 1

```

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 18:00:00 ; Search time 224 Seconds
 (without alignments)
 981.852 Million cell updates/sec

Title: US-10-662-003-4
 Perfect score: 33
 Sequence: 1 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_21:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	33	100.0	33	2	AAX61008		Aax61008	Myostatin
	2	33	100.0	33	2	AAX61006		Aax61006	Myostatin

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 19:53:11 ; Search time 74 Seconds
(without alignments)
792.696 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	33	100.0	33	3	US-08-967-089A-2	Sequence 2, Appli
	2	33	100.0	33	3	US-08-967-089A-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 20:01:25 ; Search time 406 Seconds
(without alignments)
672.142 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 33

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	33	100.0	33	7	US-10-662-003-2	Sequence 2, Appli
	2	33	100.0	33	7	US-10-662-003-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 19:33:31 ; Search time 1872 Seconds
(without alignments)
824.772 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 33

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

No matches found

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 14:29:03 ; Search time 1103.62 Seconds
(without alignments)
1699.710 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	33	100.0	33	6	AR447268	AR447268 Sequence
2	33	100.0	33	6	AR447270	AR447270 Sequence
c 3	24	72.7	1599	4	AY787760s2	AY787761 Bos grunn
c 4	24	72.7	5790	6	BD080061	BD080061 Mutation
c 5	24	72.7	6619	4	AY850105	AY850105 Bos tauru
c 6	24	72.7	6660	4	AB076403	AB076403 Bos tauru
c 7	24	72.7	6686	4	AY794986	AY794986 Bos indic
c 8	24	72.7	6691	4	AF320998	AF320998 Bos tauru

Untitled							
	9	24	72.7	145962	14	AC144373	AC144373 Felis cat
	10	24	72.7	192219	14	AC140969	AC140969 Canis fam
	11	24	72.7	192431	14	AC141853	AC141853 Bos tauru
	12	24	72.7	233029	14	AC141852	AC141852 Bos tauru
c	13	23	69.7	1240	6	AR105865	AR105865 Sequence
c	14	23	69.7	1240	6	BD080013	BD080013 Mutation
c	15	19	57.6	93281	14	AC149155	AC149155 Xenopus t
	16	19	57.6	169454	8	AP001992	AP001992 Homo sapi
	17	19	57.6	213613	14	AC013405	AC013405 Homo sapi
	18	18	54.5	1270	1	SMU78604	U78604 Streptococc
c	19	18	54.5	2743	6	AR050683	AR050683 Sequence
c	20	18	54.5	2743	6	AR105128	AR105128 Sequence
c	21	18	54.5	2743	6	AR236756	AR236756 Sequence
c	22	18	54.5	2743	6	AR237975	AR237975 Sequence
c	23	18	54.5	2743	6	AR269219	AR269219 Sequence
c	24	18	54.5	2743	6	AR381035	AR381035 Sequence
c	25	18	54.5	2743	6	AR433005	AR433005 Sequence
c	26	18	54.5	2743	6	AR477220	AR477220 Sequence
c	27	18	54.5	2743	6	AR639855	AR639855 Sequence
c	28	18	54.5	2743	6	AR655394	AR655394 Sequence
c	29	18	54.5	2743	6	AX460478	AX460478 Sequence
c	30	18	54.5	2743	6	AX960167	AX960167 Sequence
c	31	18	54.5	2823	6	CS131511	CS131511 Sequence
c	32	18	54.5	2823	8	AF104922	AF104922 Homo sapi
	33	18	54.5	7836	1	D78182	D78182 Streptococc
c	34	18	54.5	13386	1	AE014978	AE014978 Streptoco
	35	18	54.5	43877	8	AC073120	AC073120 Homo sapi
c	36	18	54.5	85722	14	AC093210	AC093210 Homo sapi
	37	18	54.5	110000	15	AP008215_225	Continuation (226
	38	18	54.5	110000	15	AP008217_255	Continuation (256
	39	18	54.5	110541	8	AC107061	AC107061 Homo sapi
	40	18	54.5	114935	14	AC035141	AC035141 Homo sapi
c	41	18	54.5	124235	8	AC020893	AC020893 Homo sapi
	42	18	54.5	132205	15	AP006162	AP006162 Oryza sat
	43	18	54.5	142790	14	AC009616	AC009616 Homo sapi
	44	18	54.5	147601	14	AC012655	AC012655 Homo sapi
	45	18	54.5	148579	8	AC092274	AC092274 Homo sapi

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:54:27 ; Search time 82.2911 Seconds
(without alignments)
712.829 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	33	100.0	33	3	US-08-967-089A-2	Sequence 2, Appli
2	33	100.0	33	3	US-08-967-089A-4	Sequence 4, Appli
c 3	23	69.7	1240	3	US-08-891-789B-3	Sequence 3, Appli
c 4	18	54.5	2743	2	US-08-525-596B-13	Sequence 13, Appl
c 5	18	54.5	2743	3	US-09-177-860A-13	Sequence 13, Appl
c 6	18	54.5	2743	3	US-09-378-238-13	Sequence 13, Appl
c 7	18	54.5	2743	3	US-09-451-501-13	Sequence 13, Appl
c 8	18	54.5	2743	3	US-09-629-938-13	Sequence 13, Appl
c 9	18	54.5	2743	3	US-09-686-344-13	Sequence 13, Appl
c 10	18	54.5	2743	3	US-09-626-896-1	Sequence 1, Appli
c 11	18	54.5	2743	3	US-09-485-046-3	Sequence 3, Appli
c 12	18	54.5	2743	3	US-10-278-803-13	Sequence 13, Appl
c 13	18	54.5	2743	3	US-09-841-730-1	Sequence 1, Appli
14	16	48.5	601	3	US-09-949-016-55628	Sequence 55628, A

					Untitled		
	15	16	48.5	601	3	US-09-949-016-55629	Sequence 55629, A
	16	16	48.5	601	3	US-09-949-016-55630	Sequence 55630, A
c	17	16	48.5	1051	3	US-09-809-545A-60	Sequence 60, Appl
	18	16	48.5	1828	3	US-09-744-900-2	Sequence 2, Appli
	19	16	48.5	3742	3	US-09-744-900-1	Sequence 1, Appli
	20	16	48.5	104520	3	US-09-949-016-13303	Sequence 13303, A
	21	16	48.5	126029	3	US-09-949-016-14731	Sequence 14731, A
c	22	16	48.5	227390	3	US-09-949-016-12201	Sequence 12201, A
c	23	16	48.5	227391	3	US-09-949-016-13365	Sequence 13365, A
c	24	16	48.5	360470	3	US-09-949-016-13173	Sequence 13173, A
	25	15	45.5	30	2	US-08-466-033-136	Sequence 136, App
	26	15	45.5	30	2	US-08-444-733-136	Sequence 136, App
	27	15	45.5	30	2	US-08-464-134-136	Sequence 136, App
	28	15	45.5	30	2	US-08-461-361-136	Sequence 136, App
	29	15	45.5	30	2	US-08-485-910-136	Sequence 136, App
c	30	15	45.5	117	3	US-09-513-999C-29295	Sequence 29295, A
	31	15	45.5	515	3	US-09-513-999C-12300	Sequence 12300, A
c	32	15	45.5	601	3	US-09-949-016-33834	Sequence 33834, A
c	33	15	45.5	601	3	US-09-949-016-155077	Sequence 155077,
c	34	15	45.5	777	3	US-09-248-796A-162	Sequence 162, App
	35	15	45.5	987	3	US-09-248-796A-5103	Sequence 5103, Ap
c	36	15	45.5	1020	3	US-09-533-559-4484	Sequence 4484, Ap
c	37	15	45.5	1689	3	US-09-248-796A-3165	Sequence 3165, Ap
c	38	15	45.5	2069	2	US-08-619-554-7	Sequence 7, Appli
	39	15	45.5	2232	3	US-09-489-039A-4139	Sequence 4139, Ap
c	40	15	45.5	2253	3	US-09-487-558B-279	Sequence 279, App
	41	15	45.5	5217	3	US-09-573-080A-201	Sequence 201, App
c	42	15	45.5	5694	3	US-09-792-024-36	Sequence 36, Appl
	43	15	45.5	20935	3	US-09-949-016-15383	Sequence 15383, A
c	44	15	45.5	36895	3	US-09-949-016-13692	Sequence 13692, A
c	45	15	45.5	37335	3	US-09-949-016-17132	Sequence 17132, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:54:27 ; Search time 82.2911 Seconds
(without alignments)
712.829 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	33	100.0	33	3	US-08-967-089A-2	Sequence 2, Appli
2	33	100.0	33	3	US-08-967-089A-4	Sequence 4, Appli
c 3	23	69.7	1240	3	US-08-891-789B-3	Sequence 3, Appli
c 4	18	54.5	2743	2	US-08-525-596B-13	Sequence 13, Appl
c 5	18	54.5	2743	3	US-09-177-860A-13	Sequence 13, Appl
c 6	18	54.5	2743	3	US-09-378-238-13	Sequence 13, Appl
c 7	18	54.5	2743	3	US-09-451-501-13	Sequence 13, Appl
c 8	18	54.5	2743	3	US-09-629-938-13	Sequence 13, Appl
c 9	18	54.5	2743	3	US-09-686-344-13	Sequence 13, Appl
c 10	18	54.5	2743	3	US-09-626-896-1	Sequence 1, Appli
c 11	18	54.5	2743	3	US-09-485-046-3	Sequence 3, Appli
c 12	18	54.5	2743	3	US-10-278-803-13	Sequence 13, Appl
c 13	18	54.5	2743	3	US-09-841-730-1	Sequence 1, Appli
14	16	48.5	601	3	US-09-949-016-55628	Sequence 55628, A

					Untitled		
	15	16	48.5	601	3	US-09-949-016-55629	Sequence 55629, A
	16	16	48.5	601	3	US-09-949-016-55630	Sequence 55630, A
c	17	16	48.5	1051	3	US-09-809-545A-60	Sequence 60, Appl
	18	16	48.5	1828	3	US-09-744-900-2	Sequence 2, Appli
	19	16	48.5	3742	3	US-09-744-900-1	Sequence 1, Appli
	20	16	48.5	104520	3	US-09-949-016-13303	Sequence 13303, A
	21	16	48.5	126029	3	US-09-949-016-14731	Sequence 14731, A
c	22	16	48.5	227390	3	US-09-949-016-12201	Sequence 12201, A
c	23	16	48.5	227391	3	US-09-949-016-13365	Sequence 13365, A
c	24	16	48.5	360470	3	US-09-949-016-13173	Sequence 13173, A
	25	15	45.5	30	2	US-08-466-033-136	Sequence 136, App
	26	15	45.5	30	2	US-08-444-733-136	Sequence 136, App
	27	15	45.5	30	2	US-08-464-134-136	Sequence 136, App
	28	15	45.5	30	2	US-08-461-361-136	Sequence 136, App
	29	15	45.5	30	2	US-08-485-910-136	Sequence 136, App
c	30	15	45.5	117	3	US-09-513-999C-29295	Sequence 29295, A
	31	15	45.5	515	3	US-09-513-999C-12300	Sequence 12300, A
c	32	15	45.5	601	3	US-09-949-016-33834	Sequence 33834, A
c	33	15	45.5	601	3	US-09-949-016-155077	Sequence 155077,
c	34	15	45.5	777	3	US-09-248-796A-162	Sequence 162, App
	35	15	45.5	987	3	US-09-248-796A-5103	Sequence 5103, Ap
c	36	15	45.5	1020	3	US-09-533-559-4484	Sequence 4484, Ap
c	37	15	45.5	1689	3	US-09-248-796A-3165	Sequence 3165, Ap
c	38	15	45.5	2069	2	US-08-619-554-7	Sequence 7, Appli
	39	15	45.5	2232	3	US-09-489-039A-4139	Sequence 4139, Ap
c	40	15	45.5	2253	3	US-09-487-558B-279	Sequence 279, App
	41	15	45.5	5217	3	US-09-573-080A-201	Sequence 201, App
c	42	15	45.5	5694	3	US-09-792-024-36	Sequence 36, Appl
	43	15	45.5	20935	3	US-09-949-016-15383	Sequence 15383, A
c	44	15	45.5	36895	3	US-09-949-016-13692	Sequence 13692, A
c	45	15	45.5	37335	3	US-09-949-016-17132	Sequence 17132, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:05:38 ; Search time 489.152 Seconds
(without alignments)
557.883 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	33	100.0	33	7	US-10-662-003-2	Sequence 2, Appli
2	33	100.0	33	7	US-10-662-003-4	Sequence 4, Appli
c 3	24	72.7	5790	6	US-10-251-115-54	Sequence 54, Appl
c 4	23	69.7	1240	6	US-10-251-115-3	Sequence 3, Appli
c 5	18	54.5	548	3	US-09-764-869-487	Sequence 487, App
c 6	18	54.5	548	5	US-10-091-504-487	Sequence 487, App
c 7	18	54.5	548	6	US-10-227-577-487	Sequence 487, App
c 8	18	54.5	2743	3	US-09-859-211-13	Sequence 13, Appl
c 9	18	54.5	2743	3	US-09-841-730-1	Sequence 1, Appli
c 10	18	54.5	2743	3	US-09-872-856-13	Sequence 13, Appl
c 11	18	54.5	2743	5	US-10-278-803-13	Sequence 13, Appl
c 12	18	54.5	2743	6	US-10-335-483-13	Sequence 13, Appl
c 13	18	54.5	2743	7	US-10-463-973-13	Sequence 13, Appl

					Untitled	
c	14	18	54.5	2743	7	US-10-456-852-3 Sequence 3, Appli
c	15	18	54.5	2743	7	US-10-662-438-1 Sequence 1, Appli
c	16	18	54.5	2743	8	US-10-665-374-1 Sequence 1, Appli
c	17	18	54.5	2743	9	US-10-997-809-13 Sequence 13, Appl
c	18	18	54.5	2743	9	US-10-991-343-13 Sequence 13, Appl
c	19	18	54.5	2823	6	US-10-366-345-27 Sequence 27, Appl
c	20	18	54.5	2823	10	US-11-019-001-2 Sequence 2, Appli
	21	17	51.5	450	4	US-09-925-065A-424443 Sequence 424443,
	22	17	51.5	593	8	US-10-643-775-1351 GENERAL INFORMATI
	23	17	51.5	597	4	US-09-925-065A-634036 Sequence 634036,
	24	17	51.5	600	9	US-10-972-079-78389 Sequence 78389, A
	25	17	51.5	600	9	US-10-972-079-78390 Sequence 78390, A
	26	17	51.5	600	9	US-10-972-079-78391 Sequence 78391, A
c	27	17	51.5	674	4	US-09-925-065A-424468 Sequence 424468,
c	28	17	51.5	807	7	US-10-424-599-51571 Sequence 51571, A
c	29	17	51.5	1398	7	US-10-477-369-44 Sequence 44, Appl
c	30	17	51.5	2235	7	US-10-424-599-51570 Sequence 51570, A
c	31	16	48.5	520	7	US-10-424-599-25906 Sequence 25906, A
c	32	16	48.5	559	4	US-09-925-065A-112237 Sequence 112237,
c	33	16	48.5	559	4	US-09-925-065A-112238 Sequence 112238,
c	34	16	48.5	559	4	US-09-925-065A-112239 Sequence 112239,
c	35	16	48.5	580	4	US-09-925-065A-615254 Sequence 615254,
	36	16	48.5	586	4	US-09-925-065A-248840 Sequence 248840,
c	37	16	48.5	593	3	US-09-876-143-29 Sequence 29, Appl
	38	16	48.5	599	9	US-10-972-079-51119 Sequence 51119, A
	39	16	48.5	600	9	US-10-972-079-18566 Sequence 18566, A
	40	16	48.5	604	4	US-09-925-065A-231436 Sequence 231436,
	41	16	48.5	606	4	US-09-925-065A-719145 Sequence 719145,
	42	16	48.5	606	4	US-09-925-065A-719146 Sequence 719146,
	43	16	48.5	969	7	US-10-424-599-4209 Sequence 4209, Ap
c	44	16	48.5	1020	5	US-10-027-632-118174 Sequence 118174,
c	45	16	48.5	1020	5	US-10-027-632-118175 Sequence 118175,

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:15:55 ; Search time 198 Seconds
(without alignments)
87.371 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4172979 seqs, 262114271 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18	54.5	2743	7	US-11-051-267-1	Sequence 1, Appli
c 2	15	45.5	836	6	US-10-750-185-64751	Sequence 64751, A
3	15	45.5	955	6	US-10-750-185-43196	Sequence 43196, A
4	15	45.5	1302	6	US-10-467-657-7359	Sequence 7359, Ap
c 5	15	45.5	1302	6	US-10-467-657-8215	Sequence 8215, Ap
6	15	45.5	1595	6	US-10-750-185-62125	Sequence 62125, A
7	15	45.5	182303	7	US-11-121-086-45	Sequence 45, Appl
c 8	14	42.4	25	7	US-11-121-849-4481	Sequence 4481, Ap
9	14	42.4	25	7	US-11-121-849-305319	Sequence 305319,
10	14	42.4	25	7	US-11-121-849-498587	Sequence 498587,
c 11	14	42.4	25	7	US-11-121-849-663970	Sequence 663970,
c 12	14	42.4	201	6	US-10-995-561-73611	Sequence 73611, A
c 13	14	42.4	201	6	US-10-995-561-80551	Sequence 80551, A

					Untitled	
	14	14	42.4	387	6	US-10-793-626-2829
c	15	14	42.4	552	6	US-10-793-626-2827
	16	14	42.4	604	7	US-11-198-847-172
	17	14	42.4	619	7	US-11-198-847-166
	18	14	42.4	763	6	US-10-750-185-39659
	19	14	42.4	864	6	US-10-750-185-41204
c	20	14	42.4	970	6	US-10-750-185-52300
	21	14	42.4	1412	6	US-10-750-185-33834
c	22	14	42.4	1426	6	US-10-750-185-54374
c	23	14	42.4	1490	6	US-10-750-185-37740
	24	14	42.4	1667	6	US-10-750-185-25855
	25	14	42.4	1698	6	US-10-750-185-58295
c	26	14	42.4	1723	6	US-10-750-185-54550
c	27	14	42.4	1808	6	US-10-750-185-53123
	28	14	42.4	1813	6	US-10-750-185-41650
	29	14	42.4	2220	6	US-10-750-185-58749
	30	14	42.4	2990	6	US-10-793-626-3899
c	31	14	42.4	3283	6	US-10-750-185-27075
c	32	14	42.4	3332	6	US-10-793-626-3928
	33	14	42.4	10405	6	US-10-995-561-83
	34	14	42.4	10412	7	US-11-055-309A-7
	35	14	42.4	36360	6	US-10-995-561-13498
	36	14	42.4	103660	6	US-10-995-561-13253
c	37	14	42.4	117431	6	US-10-995-561-13448
	38	14	42.4	130472	6	US-10-995-561-13312
c	39	14	42.4	134174	7	US-11-121-086-99
	40	14	42.4	159138	6	US-10-995-561-13230
	41	14	42.4	165883	7	US-11-112-908-18
c	42	14	42.4	172147	7	US-11-112-908-22
	43	14	42.4	175100	7	US-11-121-086-21
	44	14	42.4	187786	6	US-10-995-561-13474
	45	14	42.4	187986	6	US-10-995-561-13252

Sequence 2829, Ap
Sequence 2827, Ap
Sequence 172, App
Sequence 166, App
Sequence 39659, A
Sequence 41204, A
Sequence 52300, A
Sequence 33834, A
Sequence 54374, A
Sequence 37740, A
Sequence 25855, A
Sequence 58295, A
Sequence 54550, A
Sequence 53123, A
Sequence 41650, A
Sequence 58749, A
Sequence 3899, Ap
Sequence 27075, A
Sequence 3928, Ap
Sequence 83, Appl
Sequence 7, Appli
Sequence 13498, A
Sequence 13253, A
Sequence 13448, A
Sequence 13312, A
Sequence 99, Appl
Sequence 13230, A
Sequence 18, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 13474, A
Sequence 13252, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:29:54 ; Search time 2256.11 seconds
(without alignments)
684.351 Million cell updates/sec

Title: US-10-662-003-4
Perfect score: 33
Sequence: 1 CGCGGATCCCACAGTTTCAAATTGTTGAGGGG 33

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	72.7	797	9	CC562316	CC562316 CH240_473
c 2	19	57.6	615	1	AV754355	AV754355 AV754355
c 3	18	54.5	303	8	W24782	W24782 zb62e10.r1
c 4	18	54.5	434	9	BH386829	BH386829 AG-ND-138
5	18	54.5	477	6	CF183182	CF183182 a7d03j2.r
6	18	54.5	533	7	CN487197	CN487197 EST1843-2
7	18	54.5	592	3	BJ177385	BJ177385 BJ177385
c 8	18	54.5	633	9	BH306780	BH306780 CH230-100
9	18	54.5	722	10	CL367053	CL367053 RPCI44_36
10	18	54.5	775	10	CL613900	CL613900 OR_BB000
11	18	54.5	871	10	CW608878	CW608878 OA_ABA014
12	18	54.5	911	6	CF711208	CF711208 CCAF928TR

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	13	17	51.5	205	6	CF676819 CCAFH13TR
	14	17	51.5	287	11	AL687969 Fugu rubr
c	15	17	51.5	345	3	BI975055 sai76f11.
c	16	17	51.5	368	1	AW780982 sl87c08.y
	17	17	51.5	372	9	AQ353332 CITBI-E1-
	18	17	51.5	373	3	BP866271 BP866271
c	19	17	51.5	404	2	BE023011 sm69d04.y
c	20	17	51.5	412	8	R88840 ym97g08.s1
c	21	17	51.5	433	5	BU080499 saq25b04.
	22	17	51.5	436	6	CF183510 blg07j2.r
c	23	17	51.5	461	1	AA446796 zw89f05.r
	24	17	51.5	479	6	CF183717 b6c02j2.r
c	25	17	51.5	484	8	R88835 ym97f08.s1
	26	17	51.5	502	5	BQ454523 ke05f09.y
	27	17	51.5	526	6	CF184912 d4h08j2.r
	28	17	51.5	526	11	DE041559 Branchios
c	29	17	51.5	528	11	AL462239 T. brucei
	30	17	51.5	534	6	CF699547 CCAFH06TR
	31	17	51.5	552	6	CF183610 b5d11j2.r
c	32	17	51.5	562	11	CR351212 mte1-86H3
	33	17	51.5	563	6	CF184542 c4d10j2.r
	34	17	51.5	565	6	CF185022 e7b05j2.r
c	35	17	51.5	568	3	BI786895 sai54f12.
c	36	17	51.5	568	5	BU578597 sar59a04.
c	37	17	51.5	570	3	BM188685 saj91a05.
	38	17	51.5	577	6	CF184847 d4c08j2.r
c	39	17	51.5	589	1	AW234735 sf18f07.y
	40	17	51.5	610	6	CA483694 EST1414 M
c	41	17	51.5	630	5	BW299068 BW299068
c	42	17	51.5	638	10	CL253592 ZMMBBb060
	43	17	51.5	640	11	DE001309 Branchios
c	44	17	51.5	646	2	BF066273 st28e11.y
c	45	17	51.5	647	11	CR804313 GR0AAA25B

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 21:42:53 ; Search time 1817 Seconds
(without alignments)
406.695 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 13

Total number of hits satisfying chosen parameters: 2628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	6	AR447274	AR447274 Sequence
2	13	100.0	13	6	AR447278	AR447278 Sequence
c 3	13	100.0	25	6	A20866	A20866 oligonucleo
c 4	13	100.0	185	10	AB148455	AB148455 Homo sapi
c 5	13	100.0	200	10	AB131023	AB131023 Homo sapi
6	13	100.0	206	6	BD041665	BD041665 Sequence
7	13	100.0	206	6	AX906132	AX906132 Sequence
8	13	100.0	210	9	AF438210	AF438210 Nannospal

Untitled					
c	9	13	100.0	263 15	ATH521270 Arabidops
	10	13	100.0	272 6	BD041563 Sequence
	11	13	100.0	272 6	AX906030 Sequence
c	12	13	100.0	335 6	BD041926 Sequence
c	13	13	100.0	335 6	AX906393 Sequence
	14	13	100.0	339 15	DCU08156 Dianthus ca
	15	13	100.0	342 6	AX437071 Sequence
	16	13	100.0	400 10	BV265675 S235P6122
	17	13	100.0	407 5	AF333618 Axoclinus
	18	13	100.0	407 5	AF333620 Axoclinus
	19	13	100.0	407 5	AF333624 Axoclinus
	20	13	100.0	407 5	AF333626 Axoclinus
	21	13	100.0	407 5	AF333627 Axoclinus
	22	13	100.0	407 5	AF333648 Axoclinus
	23	13	100.0	407 5	AF333649 Axoclinus
	24	13	100.0	407 5	AF333652 Axoclinus
	25	13	100.0	407 5	AF333653 Axoclinus
	26	13	100.0	407 5	AF333654 Axoclinus
	27	13	100.0	407 5	AF333655 Axoclinus
	28	13	100.0	407 5	AF333656 Axoclinus
	29	13	100.0	407 5	AF333657 Axoclinus
	30	13	100.0	407 5	AF333658 Axoclinus
	31	13	100.0	407 5	AF333660 Axoclinus
	32	13	100.0	407 5	AF333661 Axoclinus
	33	13	100.0	407 5	AF333663 Axoclinus
	34	13	100.0	407 5	AF333664 Axoclinus
	35	13	100.0	407 5	AF333665 Axoclinus
	36	13	100.0	407 5	AF333666 Axoclinus
	37	13	100.0	407 5	AF333667 Axoclinus
	38	13	100.0	407 5	AF333670 Axoclinus
	39	13	100.0	407 5	AF333672 Axoclinus
	40	13	100.0	407 5	AF333675 Axoclinus
	41	13	100.0	408 2	CGI563477 Crassostr
c	42	13	100.0	414 2	AF328028 Beata mag
	43	13	100.0	417 6	AX644401 Sequence
	44	13	100.0	433 10	BV261965 S235P6497
c	45	13	100.0	465 10	AB146127 Homo sapi
c	46	13	100.0	474 6	CQ519173 Sequence
	47	13	100.0	528 10	BV304236 S236P6110
	48	13	100.0	534 15	AF004789 Piscidia
	49	13	100.0	536 15	AY346805 Sphagnum
	50	13	100.0	541 10	BV343703 S230P6278
	51	13	100.0	544 15	AY309688 Sphagnum
	52	13	100.0	544 15	AY346829 Sphagnum
	53	13	100.0	544 15	AY346929 Sphagnum
	54	13	100.0	544 15	AY346930 Sphagnum
	55	13	100.0	544 15	AY346931 Sphagnum
c	56	13	100.0	550 6	CQ101970 sequence
c	57	13	100.0	557 2	AY686689 Anastreph
	58	13	100.0	559 13	LM0515301 Lettuce m
c	59	13	100.0	575 15	AY092537 Arabidops
c	60	13	100.0	575 15	AY092539 Arabidops
c	61	13	100.0	575 15	AY092550 Arabidops
c	62	13	100.0	575 15	AY092551 Arabidops
c	63	13	100.0	575 15	AY092555 Arabidops
c	64	13	100.0	583 10	BV000372 S208P6763
c	65	13	100.0	587 5	AY289222 Trimeresu
c	66	13	100.0	587 5	AY289234 Trimeresu
	67	13	100.0	591 10	BV271410 S235P6225
	68	13	100.0	596 10	BV405967 S229P6261
	69	13	100.0	601 10	BV192742 sqnm17564
c	70	13	100.0	603 10	BV317154 S236P6365
	71	13	100.0	616 10	BV283239 S232P6516

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	72	13	100.0	617	10	BV329626	BV329626	S241P6147
c	73	13	100.0	630	10	BV067151	BV067151	S212P6553
c	74	13	100.0	630	10	BV332668	BV332668	S230P6154
c	75	13	100.0	631	10	BV517074	BV517074	qdu43g03.
	76	13	100.0	633	10	BV028667	BV028667	S212P6044
	77	13	100.0	633	10	BV073012	BV073012	S212P6025
c	78	13	100.0	633	10	BV241288	BV241288	S234P6407
c	79	13	100.0	636	10	BV345992	BV345992	S230P6505
c	80	13	100.0	641	10	BV400017	BV400017	S229P6397
	81	13	100.0	643	10	BV002057	BV002057	S208P6520
	82	13	100.0	645	10	BV319282	BV319282	S236P684F
c	83	13	100.0	645	10	BV420168	BV420168	S229P6441
c	84	13	100.0	656	5	AF171914	AF171914	Trimeresu
	85	13	100.0	667	10	BV582310	BV582310	G591P6255
c	86	13	100.0	667	10	BV462419	BV462419	rlv62a07.
	87	13	100.0	675	2	AY769280	AY769280	Bombyx mo
c	88	13	100.0	675	10	BV411697	BV411697	S229P6369
	89	13	100.0	675	15	AY146713	AY146713	Stellaria
c	90	13	100.0	691	10	BV357782	BV357782	S231P6288
c	91	13	100.0	694	10	BV552493	BV552493	S221P6072
c	92	13	100.0	707	8	HSA339231	AJ339231	Homo sapi
c	93	13	100.0	728	10	BV539808	BV539808	G591P6410
	94	13	100.0	734	10	BV661864	BV661864	S217P6209
	95	13	100.0	735	13	DQ115448	DQ115448	Human ade
c	96	13	100.0	742	10	BV504889	BV504889	qpq89e03.
	97	13	100.0	748	10	BV623787	BV623787	S217P6057
	98	13	100.0	754	10	BV674918	BV674918	S217P6838
	99	13	100.0	770	10	BV484647	BV484647	S215P6164
c	100	13	100.0	789	10	BV592147	BV592147	G591P5062
	101	13	100.0	797	10	BV546303	BV546303	qoe75e05.
	102	13	100.0	810	10	BV541692	BV541692	G591P5631
c	103	13	100.0	824	10	BV013155	BV013155	S212P6216
	104	13	100.0	833	10	BV502934	BV502934	qka26f12.
c	105	13	100.0	846	10	BV616679	BV616679	S215P6073
c	106	13	100.0	859	10	BV543049	BV543049	sph16d03.
c	107	13	100.0	926	10	BV520005	BV520005	G591P6019
c	108	13	100.0	1108	6	AX437104	AX437104	Sequence
	109	13	100.0	1121	13	AB023558	AB023558	Human ade
	110	13	100.0	1158	9	AY144160S1	AY144160	Mus muscu
c	111	13	100.0	1182	2	AB058623	AB058623	Metaplast
	112	13	100.0	1203	15	AF190108	AF190108	Trochoden
	113	13	100.0	1237	15	BT018373	BT018373	Zea mays
c	114	13	100.0	1338	15	BT014430	BT014430	Lycopersi
	115	13	100.0	1355	2	PYO320481	AJ320481	Plasmodiu
c	116	13	100.0	1357	2	SLMACT5	M21501	P.polycepha
	117	13	100.0	1363	15	AF544030	AF544030	Stellaria
	118	13	100.0	1363	15	AF544033	AF544033	Stellaria
c	119	13	100.0	1401	15	AY692644	AY692644	Saccharom
	120	13	100.0	1445	1	CAU76387	U76387	Corynebacte
	121	13	100.0	1476	6	CQ749500	CQ749500	Sequence
	122	13	100.0	1482	2	PFA401202	AJ401202	Plasmodiu
	123	13	100.0	1482	6	CQ824253	CQ824253	Sequence
	124	13	100.0	1545	6	AX644402	AX644402	Sequence
	125	13	100.0	1617	6	AR551608	AR551608	Sequence
c	126	13	100.0	1685	15	AF538356	AF538356	Cryptococ
	127	13	100.0	1704	15	DQ086843	DQ086843	Arabidops
	128	13	100.0	1830	1	LPS431694	AJ431694	Leuconost
c	129	13	100.0	1830	1	LPS431694	AJ431694	Leuconost
	130	13	100.0	1841	15	AY128748	AY128748	Arabidops
c	131	13	100.0	1849	2	AY094176	AY094176	Dictyoste
	132	13	100.0	1850	6	AX654858	AX654858	Sequence
c	133	13	100.0	1918	5	AY181985	AY181985	Xenopus l
	134	13	100.0	1952	9	AY144156S1	AY144156	Mus muscu

Untitled

c 135	13	100.0	1962	15	AK118814	AK118814 Arabidops
c 136	13	100.0	1985	2	AF508975	AF508975 Dictyoste
137	13	100.0	2000	6	AX595020	AX595020 Sequence
138	13	100.0	2000	6	AX818950	AX818950 Sequence
139	13	100.0	2000	6	AX829980	AX829980 Sequence
140	13	100.0	2013	6	CQ803638	CQ803638 Sequence
141	13	100.0	2013	15	AY062808	AY062808 Arabidops
142	13	100.0	2230	4	SHPGHRPPP	M82912 ovine growt
143	13	100.0	2249	15	AY338469	AY338469 Oryza sat
144	13	100.0	2342	9	BC010552	BC010552 Mus muscu
145	13	100.0	2371	15	AK102287	AK102287 Oryza sat
c 146	13	100.0	2500	15	SCU17361	U17361 Saccharomyc
147	13	100.0	2526	15	BT003012	BT003012 Arabidops
148	13	100.0	2572	9	BC025548	BC025548 Mus muscu
149	13	100.0	2595	2	D83534	D83534 Bombyx mori
150	13	100.0	2637	6	BD194408	BD194408 Secretory
151	13	100.0	2645	15	AF163822	AF163822 Arabidops
152	13	100.0	2696	6	BD192237	BD192237 Secreted
c 153	13	100.0	2709	2	PPARDB	X60788 P.polyceph
154	13	100.0	2824	15	AF344444	AF344444 Arabidops
155	13	100.0	2864	6	AX458655	AX458655 Sequence
156	13	100.0	2887	15	AY090236	AY090236 Arabidops
157	13	100.0	2981	15	AY056807	AY056807 Arabidops
158	13	100.0	3137	15	SCYBL086C	Z35847 S.cerevisia
c 159	13	100.0	3146	15	SCYJL082W	Z49357 S.cerevisia
c 160	13	100.0	3182	15	SCYJL083W	Z49358 S.cerevisia
161	13	100.0	3225	9	RNIGFIIAA	X16703 R.norvegicu
c 162	13	100.0	3351	15	AY970540	AY970540 Arabidops
c 163	13	100.0	3358	15	AY970532	AY970532 Arabidops
c 164	13	100.0	3358	15	AY970542	AY970542 Arabidops
c 165	13	100.0	3386	15	AY970541	AY970541 Arabidops
166	13	100.0	3407	9	RATRIGF	M31221 Rat insulin
c 167	13	100.0	3480	1	ASA250203	AJ250203 Aeromonas
168	13	100.0	3532	6	BD103682	BD103682 Myocardia
169	13	100.0	3532	9	RNIGF236	X13101 Rat 3.6 kb
170	13	100.0	3600	15	AY190015	AY190015 Stellaria
171	13	100.0	3603	15	AY190014	AY190014 Stellaria
c 172	13	100.0	3687	8	AF369159	AF369159 Gorilla g
c 173	13	100.0	3720	8	AF369156	AF369156 Pan trogl
c 174	13	100.0	3720	8	AF369157	AF369157 Pan trogl
c 175	13	100.0	3723	8	AF369160	AF369160 Pongo pyg
176	13	100.0	3723	15	AF544027	AF544027 Stellaria
c 177	13	100.0	3724	8	AF369158	AF369158 Gorilla g
c 178	13	100.0	3730	8	AF369147	AF369147 Homo sapi
c 179	13	100.0	3730	8	AF369154	AF369154 Homo sapi
c 180	13	100.0	3731	8	AF369120	AF369120 Homo sapi
c 181	13	100.0	3731	8	AF369121	AF369121 Homo sapi
c 182	13	100.0	3731	8	AF369122	AF369122 Homo sapi
c 183	13	100.0	3731	8	AF369123	AF369123 Homo sapi
c 184	13	100.0	3731	8	AF369124	AF369124 Homo sapi
c 185	13	100.0	3731	8	AF369125	AF369125 Homo sapi
c 186	13	100.0	3731	8	AF369126	AF369126 Homo sapi
c 187	13	100.0	3731	8	AF369127	AF369127 Homo sapi
c 188	13	100.0	3731	8	AF369128	AF369128 Homo sapi
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c 190	13	100.0	3731	8	AF369130	AF369130 Homo sapi
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c 192	13	100.0	3731	8	AF369132	AF369132 Homo sapi
c 193	13	100.0	3731	8	AF369133	AF369133 Homo sapi
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c 195	13	100.0	3731	8	AF369135	AF369135 Homo sapi
c 196	13	100.0	3731	8	AF369136	AF369136 Homo sapi
c 197	13	100.0	3731	8	AF369137	AF369137 Homo sapi

Untitled

c	198	13	100.0	3731	8	AF369138	AF369138 Homo sapi
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c	200	13	100.0	3731	8	AF369140	AF369140 Homo sapi
c	201	13	100.0	3731	8	AF369141	AF369141 Homo sapi
c	202	13	100.0	3731	8	AF369142	AF369142 Homo sapi
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c	206	13	100.0	3731	8	AF369146	AF369146 Homo sapi
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c	209	13	100.0	3731	8	AF369150	AF369150 Homo sapi
c	210	13	100.0	3731	8	AF369151	AF369151 Homo sapi
c	211	13	100.0	3731	8	AF369152	AF369152 Homo sapi
c	212	13	100.0	3731	8	AF369153	AF369153 Homo sapi
c	213	13	100.0	3731	8	AF369155	AF369155 Homo sapi
	214	13	100.0	3808	9	RNIGF238	X14833 Rat 3.8 kb
	215	13	100.0	4244	6	AR531629	AR531629 Sequence
c	216	13	100.0	4336	15	AY560610	AY560610 Cryptococ
c	217	13	100.0	4481	1	L22883	L22883 Nostoc sp.
	218	13	100.0	4563	9	RNIGF246	X14834 Rat 4.6 kb
	219	13	100.0	4569	1	BACAMYBA	M15817 Bacillus po
	220	13	100.0	4732	6	AX334597	AX334597 Sequence
	221	13	100.0	4732	8	HUMSFTP1A	M68519 Human pulmo
	222	13	100.0	4995	15	ATH510211	AJ510211 Arabidops
c	223	13	100.0	4999	15	AY372412	AY372412 Medicago
c	224	13	100.0	5238	15	HVU54767	U54767 Hordeum vul
	225	13	100.0	5420	9	MUSTLAG	D14027 Mus musculu
	226	13	100.0	6042	6	AX346846	AX346846 Sequence
	227	13	100.0	6074	6	AX347428	AX347428 Sequence
	228	13	100.0	6074	6	AX349149	AX349149 Sequence
	229	13	100.0	6074	6	AX657798	AX657798 Sequence
	230	13	100.0	6074	6	AX659072	AX659072 Sequence
	231	13	100.0	6302	15	AK120214	AK120214 Oryza sat
	232	13	100.0	6335	8	AB095938	AB095938 Homo sapi
c	233	13	100.0	6955	1	AY147019	AY147019 Pseudomon
c	234	13	100.0	7158	9	AF463746	AF463746 Mus muscu
c	235	13	100.0	7207	2	U23411	U23411 Caenorhabdi
	236	13	100.0	7252	8	HSM805807	BX537728 Homo sapi
	237	13	100.0	7267	6	CQ573329	CQ573329 Sequence
	238	13	100.0	7287	6	BD193616	BD193616 Enterococ
	239	13	100.0	8395	6	AX345077	AX345077 Sequence
	240	13	100.0	8893	14	AC014342	AC014342 Drosophil
	241	13	100.0	8898	14	AC013057	AC013057 Drosophil
	242	13	100.0	9180	6	AX346867	AX346867 Sequence
c	243	13	100.0	9363	15	AY448010S2	AY448011 Ipomoea t
	244	13	100.0	9757	13	AB016500	AB016500 Japanese
	245	13	100.0	9968	8	AF106066	AF106066 Homo sapi
	246	13	100.0	10080	13	LM0306288	AJ306288 Lettuce m
	247	13	100.0	10080	13	LMV0PP	X97704 Lettuce mos
	248	13	100.0	10478	1	AE010718	AE010718 Methanosa
c	249	13	100.0	10550	1	AE014095	AE014095 Buchnera
	250	13	100.0	10643	1	AE011581	AE011581 Leptospir
	251	13	100.0	10684	1	AE001163	AE001163 Borrelia
c	252	13	100.0	11399	1	AE010993	AE010993 Methanosa
	253	13	100.0	11603	2	AC006809	AC006809 Caenorhab
	254	13	100.0	11756	6	CQ593603	CQ593603 Sequence
	255	13	100.0	11817	1	AE006352	AE006352 Lactococc
c	256	13	100.0	11873	6	HSFACTIXG	A22491 H.sapiens f
	257	13	100.0	13594	1	AE013458	AE013458 Methanosa
c	258	13	100.0	13771	1	BA000019_64	Continuation (65 o
	259	13	100.0	13972	1	AE011327	AE011327 Leptospir
c	260	13	100.0	14996	2	AB126004	AB126004 Periplane

Untitled

261	13	100.0	15064	2	AC006713	AC006713 Caenorhab
262	13	100.0	15532	15	AB000094	AB000094 Arabidops
c 263	13	100.0	15663	2	AF125461	AF125461 Caenorhab
c 264	13	100.0	16176	1	U67571	U67571 Methanocald
c 265	13	100.0	16697	5	MTSCGENOM	Y16067 scyliorhinu
266	13	100.0	18039	8	AY206682	AY206682 Homo sapi
267	13	100.0	18585	6	AX281497	AX281497 Sequence
268	13	100.0	19914	8	AB039888	AB039888 Homo sapi
c 269	13	100.0	21009	14	AC020069	AC020069 Drosophil
c 270	13	100.0	23210	2	CET01C3	Z78413 Caenorhabdi
271	13	100.0	24248	6	CQ592415	CQ592415 Sequence
c 272	13	100.0	24874	15	AY101381	AY101381 Cryptococ
273	13	100.0	26033	14	AC164721	AC164721 Bos tauru
274	13	100.0	26173	6	AR204173	AR204173 Sequence
275	13	100.0	26173	6	AR637522	AR637522 Sequence
c 276	13	100.0	26275	2	U29377	U29377 Caenorhabdi
c 277	13	100.0	28045	14	AC012839	AC012839 Drosophil
278	13	100.0	28333	15	CR533581	CR533581 Oryza sat
c 279	13	100.0	29314	15	SPAPB24D3	AL590582 S.pombe c
280	13	100.0	30000	9	RNIGF2	X17012 Rat IGFII g
281	13	100.0	30040	14	AC015491	AC015491 Homo sapi
282	13	100.0	30762	2	CEW03G11	Z67738 Caenorhabdi
283	13	100.0	31430	2	U41025	U41025 Caenorhabdi
c 284	13	100.0	32002	8	AY692223	AY692223 Homo sapi
c 285	13	100.0	32548	6	CQ613706	CQ613706 Sequence
c 286	13	100.0	32723	2	CEM88	Z34802 Caenorhabdi
287	13	100.0	32906	9	AY038861S01	AY038861 Mus muscu
c 288	13	100.0	33099	15	SCXORFS	X83502 S.cerevisia
c 289	13	100.0	33206	6	AX409733	AX409733 Sequence
c 290	13	100.0	33206	8	HUMBFXIII	M64554 Human facto
c 291	13	100.0	34576	14	CET01A9	Z92810 Caenorhabdi
c 292	13	100.0	34716	8	DQ148409	DQ148409 Homo sapi
c 293	13	100.0	35081	2	CEF37A8	Z35600 Caenorhabdi
c 294	13	100.0	35458	8	AF536327	AF536327 Homo sapi
c 295	13	100.0	35728	2	U41022	U41022 Caenorhabdi
c 296	13	100.0	35808	14	AC017712	AC017712 Drosophil
c 297	13	100.0	36313	9	AC127607	AC127607 Rattus no
298	13	100.0	36866	5	BX928751	BX928751 Zebrafish
299	13	100.0	36891	15	AP006838	AP006838 Oryza sat
300	13	100.0	37255	2	U40933	U40933 Caenorhabdi
301	13	100.0	38026	8	AC006485	AC006485 Homo sapi
c 302	13	100.0	38059	6	CS098022	CS098022 Sequence
c 303	13	100.0	38059	6	AR390767	AR390767 Sequence
c 304	13	100.0	38059	6	AX409478	AX409478 Sequence
c 305	13	100.0	38059	8	HUMFIXG	K02402 Human coagu
306	13	100.0	38089	8	AL450364	AL450364 Human DNA
307	13	100.0	38515	15	SPAC17H9	Z98597 S.pombe chr
308	13	100.0	39454	2	AC140855	AC140855 Botryllus
309	13	100.0	39594	15	SCESTGENE	X88851 S.cerevisia
c 310	13	100.0	40359	2	CEC01H6	Z71258 Caenorhabdi
c 311	13	100.0	40750	2	CEF54B11	Z70208 Caenorhabdi
c 312	13	100.0	41389	8	AP000542	AP000542 Homo sapi
313	13	100.0	41708	6	BD245281	BD245281 Developme
314	13	100.0	41708	6	AR368770	AR368770 Sequence
315	13	100.0	41708	6	AR540873	AR540873 Sequence
316	13	100.0	41708	7	AY508486	AY508486 Bacteriop
317	13	100.0	41927	8	AL139121	AL139121 Human DNA
318	13	100.0	42300	2	U80452	U80452 Caenorhabdi
c 319	13	100.0	42422	2	CBRG21D19	AC084526 Caenorhab
c 320	13	100.0	42521	2	CEF55F3	Z81550 Caenorhabdi
321	13	100.0	42810	2	U40411	U40411 Caenorhabdi
322	13	100.0	43307	15	SPAC6F6	Z98981 S.pombe chr
c 323	13	100.0	43541	2	CBRG02A05	AC084478 Caenorhab

Untitled

324	13	100.0	43789	2	CEC10C6	Z83217 Caenorhabdi
c 325	13	100.0	44312	8	AB065453	AB065453 Homo sapi
326	13	100.0	44364	2	AC091125	AC091125 Caenorhab
c 327	13	100.0	44364	2	AC091125	AC091125 Caenorhab
c 328	13	100.0	44532	8	AC109830	AC109830 Homo sapi
329	13	100.0	45032	8	AL591049	AL591049 Human DNA
330	13	100.0	45574	14	AC020350	AC020350 Drosophil
c 331	13	100.0	46105	8	AC021085	AC021085 Homo sapi
332	13	100.0	46144	8	HSN75H12	Z84496 Human DNA s
c 333	13	100.0	46174	8	AL591599	AL591599 Human DNA
334	13	100.0	46226	2	AF101310	AF101310 Caenorhab
335	13	100.0	46612	2	AF067216	AF067216 Caenorhab
c 336	13	100.0	46872	15	AB018116	AB018116 Arabidops
337	13	100.0	47702	9	AL845484	AL845484 Mouse DNA
338	13	100.0	48423	6	BD184770	BD184770 Nucleic a
c 339	13	100.0	48613	2	CEY106G6H	AL032631 Caenorhab
340	13	100.0	48698	8	AL592171	AL592171 Human DNA
c 341	13	100.0	49249	5	CR388044	CR388044 Zebrafish
342	13	100.0	49890	15	ATF28D10	AL391254 Arabidops
343	13	100.0	50455	2	AC087081	AC087081 Caenorhab
344	13	100.0	51428	15	CR382139_20	Continuation (21 o
c 345	13	100.0	52754	14	AC099928	AC099928 Mus muscu
c 346	13	100.0	54553	8	AL603683	AL603683 Human DNA
c 347	13	100.0	54554	8	AC009500	AC009500 Homo sapi
348	13	100.0	54750	14	AC009072	AC009072 Homo sapi
349	13	100.0	54871	14	AC165619	AC165619 Bos tauru
350	13	100.0	54925	8	AL590824	AL590824 Human DNA
351	13	100.0	55069	15	YSCH9196	U11583 Saccharomyc
352	13	100.0	55310	14	AC102436	AC102436 Mus muscu
c 353	13	100.0	55790	15	AB025602	AB025602 Arabidops
354	13	100.0	56016	14	AC166373	AC166373 Bos tauru
c 355	13	100.0	56531	14	AC105232	AC105232 Homo sapi
356	13	100.0	56570	8	AL353194	AL353194 Human DNA
c 357	13	100.0	58262	8	AL163537	AL163537 Human DNA
c 358	13	100.0	58474	14	AC087846	AC087846 Homo sapi
c 359	13	100.0	59060	14	AC090034	AC090034 Homo sapi
c 360	13	100.0	59156	14	AC164764	AC164764 Bos tauru
c 361	13	100.0	60049	8	AL358853	AL358853 Human DNA
c 362	13	100.0	60932	14	AC105037	AC105037 Homo sapi
363	13	100.0	61812	8	AL591395	AL591395 Human DNA
364	13	100.0	61921	8	HSDJ892M9	AL121828 Human DNA
c 365	13	100.0	62031	9	AF021335	AF021335 Mus muscu
c 366	13	100.0	62416	14	AC073451	AC073451 Homo sapi
367	13	100.0	63087	14	AC023446	AC023446 Homo sapi
368	13	100.0	63101	15	AP003489	AP003489 Oryza sat
c 369	13	100.0	63266	8	AL607038	AL607038 Human DNA
370	13	100.0	63468	14	AC121289	AC121289 Mus muscu
c 371	13	100.0	63632	14	AC108792	AC108792 Mus muscu
372	13	100.0	63831	14	AC099931	AC099931 Mus muscu
373	13	100.0	64093	14	AC124291	AC124291 Homo sapi
374	13	100.0	64810	8	AL391535	AL391535 Human DNA
c 375	13	100.0	64837	14	AC090689	AC090689 Homo sapi
c 376	13	100.0	64893	14	AC124674	AC124674 Mus muscu
c 377	13	100.0	65147	14	AC101675	AC101675 Mus muscu
378	13	100.0	65162	14	AC022643	AC022643 Homo sapi
c 379	13	100.0	65263	14	AC113185	AC113185 Mus muscu
380	13	100.0	65547	15	AY013245	AY013245 Oryza sat
c 381	13	100.0	65691	2	PFMAL3P1	Z97348 Plasmodium
382	13	100.0	65720	14	AC091037	AC091037 Homo sapi
c 383	13	100.0	65720	14	AC091037	AC091037 Homo sapi
384	13	100.0	66229	8	AC096553	AC096553 Homo sapi
385	13	100.0	67883	15	SCE8229	U18917 saccharomyc
386	13	100.0	68007	14	AC152929	AC152929 Xenopus t

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387	13	100.0	68609	14	AC101586	AC101586 Mus muscu
388	13	100.0	68871	8	AL450265	AL450265 Human DNA
c 389	13	100.0	68997	14	AC090375	AC090375 Homo sapi
c 390	13	100.0	69203	8	AL626763	AL626763 Human DNA
391	13	100.0	69266	14	AC117763	AC117763 Mus muscu
c 392	13	100.0	70824	5	BX510906	BX510906 Zebrafish
393	13	100.0	70878	14	AC100628	AC100628 Mus muscu
394	13	100.0	71008	14	AC080024	AC080024 Homo sapi
395	13	100.0	71142	14	AC100006	AC100006 Mus muscu
396	13	100.0	72135	14	AC103316_3	Continuation (4 of
c 397	13	100.0	72374	15	AP004472	AP004472 Lotus cor
398	13	100.0	72415	14	H0102C09	AL442103 Oryza sat
399	13	100.0	74000	8	AC020650	AC020650 Homo sapi
400	13	100.0	74098	8	BS000067	BS000067 Pan trogl
401	13	100.0	74428	8	AL162495	AL162495 Human DNA
c 402	13	100.0	74613	15	AB005230	AB005230 Arabidops
403	13	100.0	75513	14	AC124819	AC124819 Mus muscu
404	13	100.0	75742	14	AC021475	AC021475 Homo sapi
c 405	13	100.0	76385	8	AC007033	AC007033 Homo sapi
c 406	13	100.0	76714	14	AC005044	AC005044 Homo sapi
c 407	13	100.0	76729	14	AC164720	AC164720 Bos tauru
c 408	13	100.0	76828	14	AP007648	AP007648 Lotus cor
c 409	13	100.0	77432	8	AL358178	AL358178 Human DNA
410	13	100.0	77546	14	AC138198	AC138198 Oryza sat
c 411	13	100.0	77618	9	BX276129	BX276129 Mouse DNA
412	13	100.0	77836	14	AP007715	AP007715 Lotus cor
413	13	100.0	78197	9	AL671896	AL671896 Mouse DNA
c 414	13	100.0	78343	14	AC155986	AC155986 Xenopus t
415	13	100.0	78600	15	SCDNCH2	X79489 S.cerevisia
c 416	13	100.0	79013	8	BS000030	BS000030 Pan trogl
417	13	100.0	79073	15	AB008271	AB008271 Arabidops
418	13	100.0	80552	8	AL356377	AL356377 Human DNA
c 419	13	100.0	80554	14	AP004143	AP004143 Oryza sat
c 420	13	100.0	80619	14	AP007459	AP007459 Lotus cor
c 421	13	100.0	80668	14	AC111021_3	Continuation (4 of
c 422	13	100.0	80678	14	AL606806	AL606806 Danio rer
c 423	13	100.0	80908	8	HS524E15	Z84485 Human DNA s
c 424	13	100.0	81701	15	AB006706	AB006706 Arabidops
425	13	100.0	81916	14	AP008094	AP008094 Lotus cor
426	13	100.0	83485	15	ATT1E3	AL162972 Arabidops
c 427	13	100.0	83700	15	AP004489	AP004489 Lotus cor
c 428	13	100.0	84307	14	AC025206	AC025206 Homo sapi
c 429	13	100.0	84615	8	AL354747	AL354747 Human DNA
c 430	13	100.0	84874	8	AL136457	AL136457 Human DNA
c 431	13	100.0	85108	8	AL358854	AL358854 Human DNA
c 432	13	100.0	85652	14	AC150118	AC150118 Gallus ga
433	13	100.0	85722	15	AC098835	AC098835 Oryza sat
434	13	100.0	86163	5	BX649400	BX649400 Zebrafish
435	13	100.0	86371	8	AL355672	AL355672 Human DNA
c 436	13	100.0	86630	15	AB005245	AB005245 Arabidops
437	13	100.0	86883	8	AL359761	AL359761 Human DNA
c 438	13	100.0	87244	15	AC093920	AC093920 Oryza sat
439	13	100.0	87351	8	AC078882	AC078882 Homo sapi
c 440	13	100.0	87640	14	AC165665	AC165665 Bos tauru
441	13	100.0	87792	14	AC159223	AC159223 Medicago
c 442	13	100.0	88198	14	AC165599	AC165599 Bos tauru
c 443	13	100.0	88292	15	T8F5	AC004512 Arabidops
444	13	100.0	88404	8	AC098485	AC098485 Homo sapi
445	13	100.0	88499	8	AP001136	AP001136 Homo sapi
446	13	100.0	88536	15	CR931811	CR931811 Medicago
c 447	13	100.0	88600	9	AL773514	AL773514 Mouse DNA
c 448	13	100.0	88709	14	AP007347	AP007347 Lotus cor
c 449	13	100.0	88725	15	AC093954	AC093954 Oryza sat

Untitled						
c 450	13	100.0	88974	14	AC072060	AC072060 Homo sapi
c 451	13	100.0	89014	8	AY675319	AY675319 Homo sapi
c 452	13	100.0	89340	8	AL355597	AL355597 Human DNA
c 453	13	100.0	89536	14	OSJN00026	AL606593 Oryza sat
454	13	100.0	90129	9	AL627078	AL627078 Mouse DNA
c 455	13	100.0	90129	14	AP007323	AP007323 Lotus cor
456	13	100.0	90176	15	ATT20K14	AL391143 Arabidops
457	13	100.0	90207	14	AP008057	AP008057 Lotus cor
458	13	100.0	90271	8	AC113402	AC113402 Homo sapi
459	13	100.0	90343	8	AC116026	AC116026 Homo sapi
460	13	100.0	90901	8	HSJ417L20	AL121974 Human DNA
461	13	100.0	90902	15	ATF28M20	AL031004 Arabidops
462	13	100.0	91039	15	AP004491	AP004491 Lotus cor
463	13	100.0	91193	15	AB025638	AB025638 Arabidops
464	13	100.0	91593	5	CR788284	CR788284 Zebrafish
c 465	13	100.0	91849	15	F6N23	AF058919 Arabidops
c 466	13	100.0	92029	14	AL357492	AL357492 Homo sapi
467	13	100.0	92060	14	AC129145	AC129145 Rattus no
c 468	13	100.0	92309	14	AC021908	AC021908 Homo sapi
469	13	100.0	92795	14	AP007985	AP007985 Lotus cor
c 470	13	100.0	93085	14	AC139050	AC139050 Mus muscu
c 471	13	100.0	93247	8	AL356264	AL356264 Human DNA
c 472	13	100.0	93443	8	HSU63630	U63630 Homo sapien
473	13	100.0	93600	8	AC010931	AC010931 Homo sapi
474	13	100.0	94170	8	AC068777	AC068777 Homo sapi
c 475	13	100.0	94202	5	BX914220	BX914220 Zebrafish
c 476	13	100.0	94749	8	HS503N11	AL031122 Human DNA
477	13	100.0	94853	14	OSIG01001	BX005352 Oryza sat
478	13	100.0	95059	14	AP008076	AP008076 Lotus cor
c 479	13	100.0	95367	15	AC152886	AC152886 Medicago
480	13	100.0	95739	14	AP004644	AP004644 Oryza sat
481	13	100.0	95866	8	AL139278	AL139278 Human DNA
c 482	13	100.0	96057	5	BX004802	BX004802 Zebrafish
c 483	13	100.0	96514	14	AL157376	AL157376 Homo sapi
c 484	13	100.0	96545	8	AC117438	AC117438 Homo sapi
485	13	100.0	96575	15	ATT1E22	AL162874 Arabidops
486	13	100.0	96916	9	AL670100	AL670100 Mouse DNA
487	13	100.0	97391	8	AL359999	AL359999 Human DNA
488	13	100.0	97705	14	AP007454	AP007454 Lotus cor
489	13	100.0	97714	15	ATF25024	AL078469 Arabidops
c 490	13	100.0	98450	8	AL354978	AL354978 Human DNA
491	13	100.0	98692	8	AL391730	AL391730 Human DNA
c 492	13	100.0	98873	14	AC015229	AC015229 Drosophil
c 493	13	100.0	99369	8	AC112140	AC112140 Homo sapi
c 494	13	100.0	99595	15	AC151742	AC151742 Medicago
c 495	13	100.0	99606	14	AP007816	AP007816 Lotus cor
c 496	13	100.0	99981	14	AC150132	AC150132 Gallus ga
c 497	13	100.0	100000	8	AB020862	AB020862 Homo sapi
c 498	13	100.0	100000	8	AP000093	AP000093 Homo sapi
c 499	13	100.0	100000	8	AP000197	AP000197 Homo sapi
500	13	100.0	100732	8	AL133347	AL133347 Human DNA

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 20:40:17 ; Search time 287 Seconds
(without alignments)
301.885 million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 13

Total number of hits satisfying chosen parameters: 130

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	13	100.0	13	2	AAX61012	Aax61012 Myostatin
	2	13	100.0	13	2	AAX61016	Aax61016 Myostatin
	3	13	100.0	206	3	AAC17920	Aac17920 Human sec
	4	13	100.0	272	3	AAC17818	Aac17818 Human sec
c	5	13	100.0	335	3	AAC18181	Aac18181 Human sec
	6	13	100.0	342	6	ABK78195	Abk78195 Bacillus
	7	13	100.0	360	13	ADT55432	Adt55432 Human car
c	8	13	100.0	368	4	AAI80223	Aai80223 Human pol
	9	13	100.0	376	12	ADP92591	Adp92591 Cotton ex

Untitled

	10	13	100.0	417	8	ABT13444	Abt13444 Breast sp
	11	13	100.0	456	9	ACH22596	Ach22596 Human adu
c	12	13	100.0	474	5	ABV51021	Abv51021 Human pro
c	13	13	100.0	481	9	ACH50060	Ach50060 Human leu
c	14	13	100.0	528	4	AAK88083	Aak88083 Human dig
c	15	13	100.0	550	4	AAI42143	Aai42143 Probe #10
	16	13	100.0	639	13	ADR62108	Adr62108 Cotton cD
	17	13	100.0	662	13	ADQ54505	Adq54505 Novel can
	18	13	100.0	717	13	ADT71330	Adt71330 Nostoc sp
	19	13	100.0	986	13	ADT18298	Adt18298 Plant CDN
c	20	13	100.0	1108	6	ABK78228	Abk78228 Bacillus
c	21	13	100.0	1357	13	ADT19965	Adt19965 Plant CDN
	22	13	100.0	1379	10	ADD30455	Add30455 Plant yie
	23	13	100.0	1379	10	ADE31562	Ade31562 Plant yie
	24	13	100.0	1379	12	ADI44428	Adi44428 Plant tra
	25	13	100.0	1482	12	ADP74629	Adp74629 Nucleotid
	26	13	100.0	1545	8	ABT13445	Abt13445 Breast sp
	27	13	100.0	1570	13	ADX12388	Adx12388 Plant ful
	28	13	100.0	1739	6	ABZ21119	Abz21119 ATP/GTP c
	29	13	100.0	1769	12	ADJ39575	Adj39575 Plant CDN
c	30	13	100.0	1817	5	ABA15256	Aba15256 Human ner
	31	13	100.0	1850	8	ADA71405	Ada71405 Rice gene
	32	13	100.0	2000	10	ACC60946	Acc60946 Gene sequ
	33	13	100.0	2000	10	ADK62449	Adk62449 Disease t
	34	13	100.0	2000	11	ACL38881	Ac138881 Rice stre
	35	13	100.0	2000	11	ACL38007	Ac138007 Rice stre
	36	13	100.0	2000	12	ADJ40900	Adj40900 Plant CDN
	37	13	100.0	2013	12	ADN72154	Adn72154 Thale cre
	38	13	100.0	2100	8	ACA28217	Aca28217 Prokaryot
	39	13	100.0	2285	12	ADQ97844	Adq97844 Mouse can
	40	13	100.0	2526	14	ADW00953	Adw00953 Nucleotid
	41	13	100.0	2625	9	ADA44992	Ada44992 Human pol
	42	13	100.0	2637	2	AAX90850	Aax90850 cDNA clon
	43	13	100.0	2696	2	AAX07424	Aax07424 Homo sapi
	44	13	100.0	2739	6	ABN90693	Abn90693 Staphyloc
	45	13	100.0	2739	13	ADS03915	Ads03915 Staphyloc
	46	13	100.0	2864	6	ABQ67171	Abq67171 Human ang
	47	13	100.0	3138	4	AAK72431	Aak72431 Human imm
	48	13	100.0	3476	3	AAC46913	Aac46913 Arabidops
	49	13	100.0	3532	6	ABI99915	Abi99915 Rat mucoc
	50	13	100.0	3578	3	AAF18304	Aaf18304 Lung canc
	51	13	100.0	4244	12	ADE77011	Ade77011 Human CDN
	52	13	100.0	4407	13	ADS47032	Ads47032 Bacterial
	53	13	100.0	4563	10	ADB53256	Adb53256 Primary r
	54	13	100.0	4563	14	ADZ60791	Adz60791 Rat Igf2
	55	13	100.0	4731	13	ADQ14721	Adq14721 Human pul
	56	13	100.0	4732	6	ABL66769	Ab166769 Lung canc
	57	13	100.0	4732	6	ABK64546	Abk64546 Human ben
	58	13	100.0	6042	6	ABL33944	Ab133944 Human imm
	59	13	100.0	6074	6	ABK33990	Abk33990 Human DNA
	60	13	100.0	6074	8	ADA20378	Ada20378 Prostate
	61	13	100.0	6074	8	ADA84185	Ada84185 Human ren
	62	13	100.0	6335	10	ADF55416	Adf55416 Human DNA
	63	13	100.0	7267	4	ABL02564	Ab102564 Drosophil
	64	13	100.0	7287	2	AAX13147	Aax13147 Enterococ
	65	13	100.0	7287	6	ABS98942	Abs98942 Enterococ
	66	13	100.0	8395	6	ABL32175	Ab132175 Human imm
	67	13	100.0	9180	6	ABL33965	Ab133965 Human imm
	68	13	100.0	9339	4	AAL02697	Aal02697 Human rep
	69	13	100.0	11756	4	ABL16080	Ab116080 Drosophil
c	70	13	100.0	11866	1	AAN40141	Aan40141 Sequence
c	71	13	100.0	11873	1	AAN40176	Aan40176 Sequence
	72	13	100.0	12987	2	AAT91324	Aat91324 Arabidops

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	73	13	100.0	14645	14	AEA61105	Aea61105 Human TU3
	74	13	100.0	18585	6	ABL34608	Ab134608 Human met
	75	13	100.0	18585	7	ADS99869	Ads99869 Bisulphit
c	76	13	100.0	22202	9	AAD58259	Aad58259 Murine tu
	77	13	100.0	24248	4	ABL15288	Ab115288 Drosophil
	78	13	100.0	26173	9	ACD19056	Acd19056 E. coli 0
	79	13	100.0	30000	13	ADR15055	Adr15055 Rat elect
c	80	13	100.0	30306	11	ACN44196	Acn44196 Mouse gen
c	81	13	100.0	32548	4	ABL29482	Ab129482 Drosophil
c	82	13	100.0	33206	6	ABN95882	Abn95882 Gene #238
	83	13	100.0	35057	8	AAL51501	Aal51501 Human pan
c	84	13	100.0	38059	4	AAF54018	Aaf54018 Human fac
c	85	13	100.0	38059	6	ABN95627	Abn95627 Gene #212
c	86	13	100.0	38059	10	ADD71098	Add71098 Human coa
	87	13	100.0	41708	3	AAA68247	Aaa68247 Bacteriop
	88	13	100.0	41708	4	AAC86106	Aac86106 Complete
c	89	13	100.0	46582	12	ADQ97900	Adq97900 Human can
	90	13	100.0	48423	10	ADC00439	Adc00439 Enterohae
	91	13	100.0	51698	12	ADQ97614	Adq97614 Mouse can
c	92	13	100.0	54169	11	ACN44838	Acn44838 Human gen
c	93	13	100.0	58226	14	ADZ13229	Adz13229 Human can
	94	13	100.0	68497	11	ACN45212	Acn45212 Mouse gen
c	95	13	100.0	87731	11	ACN44742	Acn44742 Human gen
	96	13	100.0	89014	14	AEB77360	Aeb77360 Human TGF
	97	13	100.0	92861	12	ADQ97843	Adq97843 Mouse can
c	98	13	100.0	93443	12	ADQ19270	Adq19270 Human sof
	99	13	100.0	101000	14	ADZ42285_3	Continuation (4 of
	100	13	100.0	101433	14	AEA61169_3	Continuation (4 of
c	101	13	100.0	103661	12	ADQ97712	Adq97712 Mouse can
	102	13	100.0	110000	2	AAV21209_02	Continuation (3 of
c	103	13	100.0	110000	2	AAX20248_02	Continuation (3 of
c	104	13	100.0	110000	6	ABA92787_2	Continuation (3 of
	105	13	100.0	110000	6	ABA90521_12	Continuation (13 o
c	106	13	100.0	110000	10	ADF77343_01	Continuation (2 of
	107	13	100.0	110000	12	ADQ59443_0	Adq59443 Human can
	108	13	100.0	110000	13	ABD32966_09	Continuation (10 o
c	109	13	100.0	110000	13	ABD32968_6	Continuation (7 of
	110	13	100.0	110000	14	ADZ13754_0	Adz13754 Murine ca
c	111	13	100.0	117829	12	ADQ97319	Adq97319 Human can
c	112	13	100.0	118063	12	ADQ97180	Adq97180 Mouse can
	113	13	100.0	146793	13	ABD32719	Abd32719 Mouse can
c	114	13	100.0	158091	12	ADL08119	Adl08119 Human gen
c	115	13	100.0	160271	4	AAF85116	Aaf85116 Nucleotid
c	116	13	100.0	160271	4	AAF85756	Aaf85756 Human chr
c	117	13	100.0	160271	4	AAF85750	Aaf85750 Bipolar a
c	118	13	100.0	160271	4	AAS06667	Aas06667 Human chr
c	119	13	100.0	160271	4	AAS04864	Aas04864 Human chr
c	120	13	100.0	160271	5	AAH23764	Aah23764 Human chr
c	121	13	100.0	160271	5	AAH40997	Aah40997 160kb fra
c	122	13	100.0	160271	5	AAS04858	Aas04858 Human chr
c	123	13	100.0	167739	9	AAD58258	Aad58258 Murine tu
c	124	13	100.0	174481	14	ADY75919	Ady75919 Mouse clo
c	125	13	100.0	180821	10	ADL13761	Adl13761 Osteoarth
	126	13	100.0	185695	8	ABQ77405	Abq77405 Human THB
	127	13	100.0	185695	8	AAD55693	Aad55693 Human THB
c	128	13	100.0	214019	10	ADL13809	Adl13809 Osteoarth
	129	13	100.0	254396	12	ADQ97557	Adq97557 Human can
	130	13	100.0	338702	11	ACN44042	Acn44042 Human gen

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 21:59:08 ; Search time 98 Seconds
(without alignments)
235.799 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 13

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	3	US-08-967-089A-8	Sequence 8, Appli
2	13	100.0	13	3	US-08-967-089A-12	Sequence 12, Appl
3	13	100.0	206	3	US-09-513-999C-21995	Sequence 21995, A
4	13	100.0	272	3	US-09-513-999C-21893	Sequence 21893, A
c 5	13	100.0	335	3	US-09-513-999C-22256	Sequence 22256, A
c 6	13	100.0	601	3	US-09-949-016-17822	Sequence 17822, A
7	13	100.0	601	3	US-09-949-016-60845	Sequence 60845, A
c 8	13	100.0	601	3	US-09-949-016-109582	Sequence 109582,
c 9	13	100.0	601	3	US-09-949-016-152975	Sequence 152975,
10	13	100.0	1617	3	US-09-248-796A-6739	Sequence 6739, Ap
11	13	100.0	2739	3	US-09-134-001C-156	Sequence 156, App
12	13	100.0	4244	3	US-09-919-039-176	Sequence 176, App
13	13	100.0	6490	3	US-09-949-016-12342	Sequence 12342, A
14	13	100.0	6491	3	US-09-949-016-15320	Sequence 15320, A

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c	15	13	100.0	11890	3	US-09-949-016-13794	Sequence 13794, A
	16	13	100.0	26173	3	US-09-453-702B-69	Sequence 69, Appl
	17	13	100.0	26173	3	US-10-114-170-69	Sequence 69, Appl
c	18	13	100.0	32039	3	US-09-949-016-16647	Sequence 16647, A
c	19	13	100.0	32043	3	US-09-949-016-12028	Sequence 12028, A
c	20	13	100.0	36028	3	US-09-949-016-14761	Sequence 14761, A
c	21	13	100.0	36755	3	US-09-949-016-16994	Sequence 16994, A
c	22	13	100.0	38059	3	US-09-328-925-4	Sequence 4, Appli
c	23	13	100.0	39433	3	US-09-949-016-12014	Sequence 12014, A
	24	13	100.0	41708	3	US-09-470-512A-3	Sequence 3, Appli
	25	13	100.0	41708	3	US-09-676-519-18	Sequence 18, Appl
	26	13	100.0	54531	3	US-09-949-016-16267	Sequence 16267, A
	27	13	100.0	60110	3	US-09-949-016-17338	Sequence 17338, A
	28	13	100.0	60110	3	US-09-949-016-17339	Sequence 17339, A
	29	13	100.0	61083	3	US-09-949-016-14144	Sequence 14144, A
	30	13	100.0	61083	3	US-09-949-016-14145	Sequence 14145, A
	31	13	100.0	64190	3	US-09-949-016-14712	Sequence 14712, A
	32	13	100.0	64190	3	US-09-949-016-14713	Sequence 14713, A
	33	13	100.0	70947	3	US-09-949-016-15165	Sequence 15165, A
c	34	13	100.0	75394	3	US-09-949-016-11754	Sequence 11754, A
	35	13	100.0	107458	3	US-09-949-016-15687	Sequence 15687, A
c	36	13	100.0	117410	3	US-09-949-016-12262	Sequence 12262, A
c	37	13	100.0	123463	3	US-09-949-016-17078	Sequence 17078, A
c	38	13	100.0	140925	3	US-09-949-016-11777	Sequence 11777, A
c	39	13	100.0	140982	3	US-09-949-016-16295	Sequence 16295, A
c	40	13	100.0	152524	3	US-09-949-016-12683	Sequence 12683, A
c	41	13	100.0	152524	3	US-09-949-016-13194	Sequence 13194, A
c	42	13	100.0	166698	3	US-09-949-016-16038	Sequence 16038, A
	43	13	100.0	256171	3	US-09-949-016-12822	Sequence 12822, A
	44	13	100.0	256176	3	US-09-949-016-15524	Sequence 15524, A
	45	13	100.0	276237	3	US-09-949-016-17504	Sequence 17504, A
	46	13	100.0	283538	3	US-09-949-016-13506	Sequence 13506, A
c	47	13	100.0	390416	3	US-09-949-016-16923	Sequence 16923, A
c	48	13	100.0	640681	3	US-09-790-988-1	Sequence 1, Appli
	49	13	100.0	1664976	3	US-08-916-421B-1	Sequence 1, Appli
	50	13	100.0	1664976	3	US-09-692-570-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 22:04:37 ; Search time 481 seconds
(without alignments)
223.497 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 13

Total number of hits satisfying chosen parameters: 252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_NA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	7	US-10-662-003-8	Sequence 8, Appli
2	13	100.0	13	7	US-10-662-003-12	Sequence 12, Appl
3	13	100.0	25	7	US-10-719-956-332547	Sequence 332547,
c 4	13	100.0	185	8	US-10-674-124A-668	Sequence 668, App
c 5	13	100.0	200	8	US-10-674-124A-830	Sequence 830, App
6	13	100.0	201	8	US-10-719-993-44196	Sequence 44196, A
7	13	100.0	201	8	US-10-719-993-49906	Sequence 49906, A
8	13	100.0	339	4	US-09-925-065A-502367	Sequence 502367,
9	13	100.0	339	4	US-09-925-065A-502368	Sequence 502368,
10	13	100.0	342	3	US-09-974-300-5486	Sequence 5486, Ap
c 11	13	100.0	358	4	US-09-925-065A-138421	Sequence 138421,
12	13	100.0	360	8	US-10-727-664-16	Sequence 16, Appl
c 13	13	100.0	364	4	US-09-925-065A-565486	Sequence 565486,

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	14	13	100.0	367	4	US-09-925-065A-806575
	15	13	100.0	372	5	US-10-027-632-56354
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C	17	13	100.0	372	5	US-10-027-632-274544
	18	13	100.0	372	5	US-10-027-632-299463
	19	13	100.0	372	6	US-10-027-632-56354
C	20	13	100.0	372	6	US-10-027-632-274543
C	21	13	100.0	372	6	US-10-027-632-274544
	22	13	100.0	372	6	US-10-027-632-299463
	23	13	100.0	376	3	US-09-732-627A-1602
C	24	13	100.0	416	5	US-10-027-632-291518
C	25	13	100.0	416	5	US-10-027-632-291519
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C	27	13	100.0	416	6	US-10-027-632-291519
	28	13	100.0	417	3	US-09-989-890-159
	29	13	100.0	453	7	US-10-424-599-133934
	30	13	100.0	456	3	US-09-918-995-9808
C	31	13	100.0	465	8	US-10-674-124A-2131
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C	34	13	100.0	484	4	US-09-925-065A-302871
	35	13	100.0	485	4	US-09-925-065A-502369
	36	13	100.0	492	4	US-09-925-065A-658167
	37	13	100.0	492	4	US-09-925-065A-658168
	38	13	100.0	493	4	US-09-925-065A-448418
	39	13	100.0	493	4	US-09-925-065A-728664
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	45	13	100.0	516	7	US-10-437-963-75673
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	47	13	100.0	525	4	US-09-925-065A-271095
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	51	13	100.0	534	4	US-09-925-065A-175865
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C	53	13	100.0	537	4	US-09-925-065A-147621
C	54	13	100.0	541	4	US-09-925-065A-454994
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	56	13	100.0	542	4	US-09-925-065A-658687
C	57	13	100.0	546	4	US-09-925-065A-276280
	58	13	100.0	547	4	US-09-925-065A-543188
	59	13	100.0	547	7	US-10-424-599-128509
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C	67	13	100.0	555	4	US-09-925-065A-29221
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	69	13	100.0	560	4	US-09-925-065A-752609
	70	13	100.0	563	4	US-09-925-065A-954103
	71	13	100.0	564	7	US-10-424-599-13337
	72	13	100.0	566	4	US-09-925-065A-21335
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c 77	13	100.0	581	5	US-10-027-632-57838	Sequence 57838, A
c 78	13	100.0	581	5	US-10-027-632-57839	Sequence 57839, A
c 79	13	100.0	581	5	US-10-027-632-294994	Sequence 294994,
c 80	13	100.0	581	5	US-10-027-632-294995	Sequence 294995,
c 81	13	100.0	581	6	US-10-027-632-57838	Sequence 57838, A
c 82	13	100.0	581	6	US-10-027-632-57839	Sequence 57839, A
c 83	13	100.0	581	6	US-10-027-632-294994	Sequence 294994,
c 84	13	100.0	581	6	US-10-027-632-294995	Sequence 294995,
85	13	100.0	588	4	US-09-925-065A-688226	Sequence 688226,
86	13	100.0	589	4	US-09-925-065A-163745	Sequence 163745,
c 87	13	100.0	589	4	US-09-925-065A-453657	Sequence 453657,
c 88	13	100.0	589	4	US-09-925-065A-453658	Sequence 453658,
c 89	13	100.0	589	5	US-10-027-632-251268	Sequence 251268,
c 90	13	100.0	589	5	US-10-027-632-251269	Sequence 251269,
c 91	13	100.0	589	6	US-10-027-632-251268	Sequence 251268,
c 92	13	100.0	589	6	US-10-027-632-251269	Sequence 251269,
c 93	13	100.0	592	4	US-09-925-065A-831779	Sequence 831779,
c 94	13	100.0	592	4	US-09-925-065A-908243	Sequence 908243,
95	13	100.0	594	5	US-10-027-632-269788	Sequence 269788,
96	13	100.0	594	6	US-10-027-632-269788	Sequence 269788,
c 97	13	100.0	597	4	US-09-925-065A-149293	Sequence 149293,
c 98	13	100.0	597	4	US-09-925-065A-149294	Sequence 149294,
99	13	100.0	597	4	US-09-925-065A-900760	Sequence 900760,
c 100	13	100.0	598	4	US-09-925-065A-323454	Sequence 323454,
101	13	100.0	600	9	US-10-972-079-35811	Sequence 35811, A
102	13	100.0	603	4	US-09-925-065A-356239	Sequence 356239,
c 103	13	100.0	603	4	US-09-925-065A-893274	Sequence 893274,
c 104	13	100.0	603	4	US-09-925-065A-893275	Sequence 893275,
c 105	13	100.0	603	4	US-09-925-065A-915409	Sequence 915409,
106	13	100.0	610	4	US-09-925-065A-388804	Sequence 388804,
107	13	100.0	612	5	US-10-027-632-5932	Sequence 5932, Ap
108	13	100.0	612	5	US-10-027-632-5933	Sequence 5933, Ap
109	13	100.0	612	6	US-10-027-632-5932	Sequence 5932, Ap
110	13	100.0	612	6	US-10-027-632-5933	Sequence 5933, Ap
111	13	100.0	615	5	US-10-027-632-188274	Sequence 188274,
112	13	100.0	615	6	US-10-027-632-188274	Sequence 188274,
c 113	13	100.0	619	5	US-10-027-632-3101	Sequence 3101, Ap
c 114	13	100.0	619	6	US-10-027-632-3101	Sequence 3101, Ap
115	13	100.0	620	4	US-09-925-065A-419719	Sequence 419719,
c 116	13	100.0	624	4	US-09-925-065A-853327	Sequence 853327,
c 117	13	100.0	624	4	US-09-925-065A-853328	Sequence 853328,
c 118	13	100.0	625	4	US-09-925-065A-793349	Sequence 793349,
c 119	13	100.0	627	4	US-09-925-065A-553792	Sequence 553792,
c 120	13	100.0	627	4	US-09-925-065A-553793	Sequence 553793,
121	13	100.0	629	4	US-09-925-065A-487601	Sequence 487601,
c 122	13	100.0	630	4	US-09-925-065A-188912	Sequence 188912,
c 123	13	100.0	630	4	US-09-925-065A-188913	Sequence 188913,
124	13	100.0	631	5	US-10-027-632-279800	Sequence 279800,
125	13	100.0	631	5	US-10-027-632-279801	Sequence 279801,
126	13	100.0	631	6	US-10-027-632-279800	Sequence 279800,
127	13	100.0	631	6	US-10-027-632-279801	Sequence 279801,
c 128	13	100.0	633	4	US-09-925-065A-783213	Sequence 783213,
c 129	13	100.0	636	4	US-09-925-065A-703470	Sequence 703470,
130	13	100.0	639	8	US-10-767-795-2889	Sequence 2889, Ap
c 131	13	100.0	643	4	US-09-925-065A-809411	Sequence 809411,
132	13	100.0	651	5	US-10-027-632-208067	Sequence 208067,
133	13	100.0	651	5	US-10-027-632-208068	Sequence 208068,
134	13	100.0	651	5	US-10-027-632-208069	Sequence 208069,
135	13	100.0	651	5	US-10-027-632-208070	Sequence 208070,
136	13	100.0	651	6	US-10-027-632-208067	Sequence 208067,
137	13	100.0	651	6	US-10-027-632-208068	Sequence 208068,
138	13	100.0	651	6	US-10-027-632-208069	Sequence 208069,
139	13	100.0	651	6	US-10-027-632-208070	Sequence 208070,

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c 140	13	100.0	653	5	US-10-027-632-208876	Sequence 208876,
c 141	13	100.0	653	5	US-10-027-632-208877	Sequence 208877,
c 142	13	100.0	653	6	US-10-027-632-208876	Sequence 208876,
c 143	13	100.0	653	6	US-10-027-632-208877	Sequence 208877,
c 144	13	100.0	696	4	US-09-925-065A-547319	Sequence 547319,
c 145	13	100.0	712	5	US-10-027-632-137495	Sequence 137495,
c 146	13	100.0	712	5	US-10-027-632-137496	Sequence 137496,
c 147	13	100.0	712	6	US-10-027-632-137495	Sequence 137495,
c 148	13	100.0	712	6	US-10-027-632-137496	Sequence 137496,
149	13	100.0	717	8	US-10-810-352-81	Sequence 81, Appl
150	13	100.0	828	4	US-09-925-065A-708601	Sequence 708601,
151	13	100.0	828	4	US-09-925-065A-708602	Sequence 708602,
152	13	100.0	886	5	US-10-027-632-33820	Sequence 33820, A
153	13	100.0	886	6	US-10-027-632-33820	Sequence 33820, A
c 154	13	100.0	902	7	US-10-437-963-32379	Sequence 32379, A
155	13	100.0	966	4	US-09-925-065A-63348	Sequence 63348, A
156	13	100.0	986	8	US-10-739-930-3624	Sequence 3624, Ap
c 157	13	100.0	1108	3	US-09-974-300-5519	Sequence 5519, Ap
c 158	13	100.0	1173	5	US-10-027-632-116754	Sequence 116754,
c 159	13	100.0	1173	6	US-10-027-632-116754	Sequence 116754,
160	13	100.0	1215	4	US-09-925-065A-701450	Sequence 701450,
c 161	13	100.0	1226	5	US-10-027-632-116735	Sequence 116735,
c 162	13	100.0	1226	6	US-10-027-632-116735	Sequence 116735,
c 163	13	100.0	1339	4	US-09-925-065A-717445	Sequence 717445,
c 164	13	100.0	1339	4	US-09-925-065A-717446	Sequence 717446,
c 165	13	100.0	1339	4	US-09-925-065A-717447	Sequence 717447,
c 166	13	100.0	1357	8	US-10-739-930-5291	Sequence 5291, Ap
167	13	100.0	1367	7	US-10-424-599-128506	Sequence 128506,
168	13	100.0	1379	6	US-10-225-066A-487	Sequence 487, App
169	13	100.0	1379	7	US-10-225-067-129	Sequence 129, App
170	13	100.0	1379	7	US-10-374-780A-2891	Sequence 2891, Ap
171	13	100.0	1379	9	US-10-225-066A-487	Sequence 487, App
172	13	100.0	1384	7	US-10-424-599-87493	Sequence 87493, A
c 173	13	100.0	1474	4	US-09-925-065A-696854	Sequence 696854,
c 174	13	100.0	1474	4	US-09-925-065A-696855	Sequence 696855,
c 175	13	100.0	1474	4	US-09-925-065A-696856	Sequence 696856,
c 176	13	100.0	1474	4	US-09-925-065A-696857	Sequence 696857,
177	13	100.0	1545	3	US-09-989-890-160	Sequence 160, App
178	13	100.0	1570	7	US-10-425-114-6963	Sequence 6963, Ap
179	13	100.0	1575	4	US-09-925-065A-59742	Sequence 59742, A
180	13	100.0	1769	7	US-10-260-238-575	Sequence 575, App
c 181	13	100.0	1958	5	US-10-027-632-97156	Sequence 97156, A
c 182	13	100.0	1958	5	US-10-027-632-97157	Sequence 97157, A
c 183	13	100.0	1958	5	US-10-027-632-97158	Sequence 97158, A
c 184	13	100.0	1958	6	US-10-027-632-97156	Sequence 97156, A
c 185	13	100.0	1958	6	US-10-027-632-97157	Sequence 97157, A
c 186	13	100.0	1958	6	US-10-027-632-97158	Sequence 97158, A
187	13	100.0	2000	7	US-10-260-238-1900	Sequence 1900, Ap
188	13	100.0	2100	7	US-10-282-122A-16087	Sequence 16087, A
189	13	100.0	2480	7	US-10-437-963-26236	Sequence 26236, A
190	13	100.0	2687	8	US-10-425-115-97027	Sequence 97027, A
191	13	100.0	2696	3	US-09-746-783-35	Sequence 35, Appl
192	13	100.0	2739	7	US-10-724-972A-3210	Sequence 3210, Ap
193	13	100.0	2864	7	US-10-433-793-201	Sequence 201, App
194	13	100.0	2890	7	US-10-437-963-13423	Sequence 13423, A
c 195	13	100.0	3383	7	US-10-437-963-93586	Sequence 93586, A
196	13	100.0	3532	6	US-10-258-666-1	Sequence 1, Appli
197	13	100.0	3540	7	US-10-437-963-40624	Sequence 40624, A
198	13	100.0	3578	3	US-09-925-302-323	Sequence 323, App
199	13	100.0	3578	3	US-09-925-302-323	Sequence 323, App
200	13	100.0	4244	3	US-09-919-039-176	Sequence 176, App
201	13	100.0	4407	6	US-10-369-493-25462	Sequence 25462, A
202	13	100.0	4563	9	US-10-764-420-515	Sequence 515, App

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203	13	100.0	4731	7	US-10-686-786-1	Sequence 1, Appli
204	13	100.0	4732	3	US-09-954-456-2079	Sequence 2079, Ap
205	13	100.0	4732	3	US-09-960-706-699	Sequence 699, App
206	13	100.0	4732	3	US-09-873-319-441	Sequence 441, App
207	13	100.0	4732	9	US-10-843-641A-5106	Sequence 5106, Ap
208	13	100.0	6042	6	US-10-311-455-1917	Sequence 1917, Ap
209	13	100.0	6074	5	US-10-172-086-43	Sequence 43, Appl
210	13	100.0	6074	7	US-10-311-507-75	Sequence 75, Appl
211	13	100.0	6074	8	US-10-480-846-43	Sequence 43, Appl
212	13	100.0	7267	10	US-11-097-143-1087	Sequence 1087, Ap
213	13	100.0	7287	3	US-09-070-927A-210	Sequence 210, App
214	13	100.0	8395	6	US-10-311-455-148	Sequence 148, App
215	13	100.0	9180	6	US-10-311-455-1938	Sequence 1938, Ap
216	13	100.0	9339	3	US-09-764-891-5385	Sequence 5385, Ap
217	13	100.0	11756	10	US-11-097-143-21361	Sequence 21361, A
218	13	100.0	14645	9	US-10-737-082-15	Sequence 15, Appl
219	13	100.0	14645	9	US-10-765-790-15	Sequence 15, Appl
220	13	100.0	18585	6	US-10-240-485-161	Sequence 161, App
221	13	100.0	24248	10	US-11-097-143-20173	Sequence 20173, A
222	13	100.0	26173	5	US-10-114-170-69	Sequence 69, Appl
223	13	100.0	30000	7	US-10-664-705-88	Sequence 88, Appl
c 224	13	100.0	30306	5	US-10-087-192-523	Sequence 523, App
c 225	13	100.0	32548	10	US-11-097-143-41464	Sequence 41464, A
c 226	13	100.0	33206	3	US-09-880-107-2380	Sequence 2380, Ap
c 227	13	100.0	38059	3	US-09-880-107-2125	Sequence 2125, Ap
c 228	13	100.0	40045	8	US-10-741-600-17795	Sequence 17795, A
c 229	13	100.0	44752	8	US-10-741-600-17553	Sequence 17553, A
230	13	100.0	50679	8	US-10-719-993-6992	Sequence 6992, Ap
231	13	100.0	52899	6	US-10-085-117-148	Sequence 148, App
c 232	13	100.0	54169	5	US-10-087-192-1486	Sequence 1486, Ap
233	13	100.0	68497	5	US-10-087-192-2047	Sequence 2047, Ap
c 234	13	100.0	87731	5	US-10-087-192-1342	Sequence 1342, Ap
c 235	13	100.0	93443	8	US-10-723-860-2089	Sequence 2089, Ap
c 236	13	100.0	93443	9	US-10-756-149-1950	Sequence 1950, Ap
237	13	100.0	146793	8	US-10-388-838-65	Sequence 65, Appl
c 238	13	100.0	149000	8	US-10-741-600-17780	Sequence 17780, A
239	13	100.0	156318	8	US-10-741-600-17574	Sequence 17574, A
c 240	13	100.0	158091	7	US-10-235-192A-38	Sequence 38, Appl
241	13	100.0	171843	9	US-10-981-277-44	Sequence 44, Appl
c 242	13	100.0	174481	9	US-10-662-613-6	Sequence 6, Appli
243	13	100.0	185695	5	US-10-020-141-11	Sequence 11, Appl
244	13	100.0	185695	5	US-10-017-721-1	Sequence 1, Appli
245	13	100.0	188169	9	US-10-981-277-45	Sequence 45, Appl
c 246	13	100.0	195071	8	US-10-741-600-17991	Sequence 17991, A
247	13	100.0	338702	5	US-10-087-192-292	Sequence 292, App
248	13	100.0	352938	7	US-10-322-696-79	Sequence 79, Appl
249	13	100.0	401433	9	US-10-737-082-79	Sequence 79, Appl
250	13	100.0	401433	9	US-10-765-790-79	Sequence 79, Appl
c 251	13	100.0	640681	3	US-09-790-988-1	Sequence 1, Appli
252	13	100.0	1790242	8	US-10-719-993-6940	Sequence 6940, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 22:09:34 ; Search time 174 Seconds
(without alignments)
39.167 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4172979 seqs, 262114271 residues

Word size : 13

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	100.0	600	6	US-10-750-185-819	Sequence 819, App
2	13	100.0	723	6	US-10-750-185-28682	Sequence 28682, A
c 3	13	100.0	1034	6	US-10-750-185-56502	Sequence 56502, A
4	13	100.0	1300	7	US-11-112-908-255	Sequence 255, App
c 5	13	100.0	1408	6	US-10-750-185-29501	Sequence 29501, A
c 6	13	100.0	1486	6	US-10-750-185-64765	Sequence 64765, A
7	13	100.0	1709	6	US-10-750-185-38811	Sequence 38811, A
c 8	13	100.0	1905	6	US-10-750-185-46767	Sequence 46767, A
9	13	100.0	2670	6	US-10-750-185-30821	Sequence 30821, A
10	13	100.0	2696	6	US-10-689-742-35	Sequence 35, Appl
11	13	100.0	150437	7	US-11-112-908-44	Sequence 44, Appl
12	13	100.0	150491	7	US-11-112-908-46	Sequence 46, Appl
c 13	13	100.0	165627	7	US-11-121-086-89	Sequence 89, Appl

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c 14 13 100.0 195235 6 US-10-995-561-13495 Sequence 13495, A

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 21:45:23 ; Search time 2205 Seconds
(without alignments)
275.842 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 13

Total number of hits satisfying chosen parameters: 1477

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 14:29:03 ; Search time 434.76 Seconds
(without alignments)
1699.710 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	6	AR447274	AR447274 Sequence
2	13	100.0	13	6	AR447278	AR447278 Sequence
c 3	13	100.0	25	6	A20866	A20866 oligonucleo
c 4	13	100.0	185	10	AB148455	AB148455 Homo sapi
c 5	13	100.0	200	10	AB131023	AB131023 Homo sapi
6	13	100.0	206	6	BD041665	BD041665 Sequence
7	13	100.0	206	6	AX906132	AX906132 Sequence
8	13	100.0	210	9	AF438210	AF438210 Nannospal

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c	9	13	100.0	263	15	ATH521270	AJ521270 Arabidops
	10	13	100.0	272	6	BD041563	BD041563 Sequence
	11	13	100.0	272	6	AX906030	AX906030 Sequence
c	12	13	100.0	335	6	BD041926	BD041926 Sequence
c	13	13	100.0	335	6	AX906393	AX906393 Sequence
	14	13	100.0	339	15	DCU08156	U08156 Dianthus ca
	15	13	100.0	342	6	AX437071	AX437071 Sequence
	16	13	100.0	400	10	BV265675	BV265675 S235P6122
	17	13	100.0	407	5	AF333618	AF333618 Axoclinus
	18	13	100.0	407	5	AF333620	AF333620 Axoclinus
	19	13	100.0	407	5	AF333624	AF333624 Axoclinus
	20	13	100.0	407	5	AF333626	AF333626 Axoclinus
	21	13	100.0	407	5	AF333627	AF333627 Axoclinus
	22	13	100.0	407	5	AF333648	AF333648 Axoclinus
	23	13	100.0	407	5	AF333649	AF333649 Axoclinus
	24	13	100.0	407	5	AF333652	AF333652 Axoclinus
	25	13	100.0	407	5	AF333653	AF333653 Axoclinus
	26	13	100.0	407	5	AF333654	AF333654 Axoclinus
	27	13	100.0	407	5	AF333655	AF333655 Axoclinus
	28	13	100.0	407	5	AF333656	AF333656 Axoclinus
	29	13	100.0	407	5	AF333657	AF333657 Axoclinus
	30	13	100.0	407	5	AF333658	AF333658 Axoclinus
	31	13	100.0	407	5	AF333660	AF333660 Axoclinus
	32	13	100.0	407	5	AF333661	AF333661 Axoclinus
	33	13	100.0	407	5	AF333663	AF333663 Axoclinus
	34	13	100.0	407	5	AF333664	AF333664 Axoclinus
	35	13	100.0	407	5	AF333665	AF333665 Axoclinus
	36	13	100.0	407	5	AF333666	AF333666 Axoclinus
	37	13	100.0	407	5	AF333667	AF333667 Axoclinus
	38	13	100.0	407	5	AF333670	AF333670 Axoclinus
	39	13	100.0	407	5	AF333672	AF333672 Axoclinus
	40	13	100.0	407	5	AF333675	AF333675 Axoclinus
	41	13	100.0	408	2	CGI563477	AJ563477 Crassostr
c	42	13	100.0	414	2	AF328028	AF328028 Beata mag
	43	13	100.0	417	6	AX644401	AX644401 Sequence
	44	13	100.0	433	10	BV261965	BV261965 S235P6497
c	45	13	100.0	465	10	AB146127	AB146127 Homo sapi

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 14:23:33 ; Search time 104.658 Seconds
(without alignments)
827.847 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	2	AAX61012	Aax61012 Myostatin
2	13	100.0	13	2	AAX61016	Aax61016 Myostatin
3	13	100.0	206	3	AAC17920	Aac17920 Human sec
4	13	100.0	272	3	AAC17818	Aac17818 Human sec
c 5	13	100.0	335	3	AAC18181	Aac18181 Human sec
6	13	100.0	342	6	ABK78195	Abk78195 Bacillus
7	13	100.0	360	13	ADT55432	Adt55432 Human car
c 8	13	100.0	368	4	AAI80223	Aai80223 Human pol
9	13	100.0	376	12	ADP92591	Adp92591 Cotton ex

Untitled							
	10	13	100.0	417	8	ABT13444	Abt13444 Breast sp
	11	13	100.0	456	9	ACH22596	Ach22596 Human adu
c	12	13	100.0	474	5	ABV51021	Abv51021 Human pro
c	13	13	100.0	481	9	ACH50060	Ach50060 Human leu
c	14	13	100.0	528	4	AAK88083	Aak88083 Human dig
c	15	13	100.0	550	4	AAI42143	Aai42143 Probe #10
	16	13	100.0	639	13	ADR62108	Adr62108 Cotton CD
	17	13	100.0	662	13	ADQ54505	Adq54505 Novel can
	18	13	100.0	717	13	ADT71330	Adt71330 Nostoc sp
	19	13	100.0	986	13	ADT18298	Adt18298 Plant cDN
c	20	13	100.0	1108	6	ABK78228	Abk78228 Bacillus
c	21	13	100.0	1357	13	ADT19965	Adt19965 Plant cDN
	22	13	100.0	1379	10	ADD30455	Add30455 Plant yie
	23	13	100.0	1379	10	ADE31562	Ade31562 Plant yie
	24	13	100.0	1379	12	ADI44428	Adi44428 Plant tra
	25	13	100.0	1482	12	ADP74629	Adp74629 Nucleotid
	26	13	100.0	1545	8	ABT13445	Abt13445 Breast sp
	27	13	100.0	1570	13	ADX12388	Adx12388 Plant ful
	28	13	100.0	1739	6	ABZ21119	Abz21119 ATP/GTP c
	29	13	100.0	1769	12	ADJ39575	Adj39575 Plant cDN
c	30	13	100.0	1817	5	ABA15256	Aba15256 Human ner
	31	13	100.0	1850	8	ADA71405	Ada71405 Rice gene
	32	13	100.0	2000	10	ACC60946	Acc60946 Gene sequ
	33	13	100.0	2000	10	ADK62449	Adk62449 Disease t
	34	13	100.0	2000	11	ACL38881	Ac138881 Rice stre
	35	13	100.0	2000	11	ACL38007	Ac138007 Rice stre
	36	13	100.0	2000	12	ADJ40900	Adj40900 Plant cDN
	37	13	100.0	2013	12	ADN72154	Adn72154 Thale cre
	38	13	100.0	2100	8	ACA28217	Aca28217 Prokaryot
	39	13	100.0	2285	12	ADQ97844	Adq97844 Mouse can
	40	13	100.0	2526	14	ADW00953	Adw00953 Nucleotid
	41	13	100.0	2625	9	ADA44992	Ada44992 Human pol
	42	13	100.0	2637	2	AAX90850	Aax90850 cDNA clon
	43	13	100.0	2696	2	AAX07424	Aax07424 Homo sapi
	44	13	100.0	2739	6	ABN90693	Abn90693 Staphyloc
	45	13	100.0	2739	13	ADS03915	Ads03915 staphyloc

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:54:27 ; Search time 32.4177 Seconds
(without alignments)
712.829 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	3	US-08-967-089A-8	Sequence 8, Appli
2	13	100.0	13	3	US-08-967-089A-12	Sequence 12, Appl
3	13	100.0	206	3	US-09-513-999C-21995	Sequence 21995, A
4	13	100.0	272	3	US-09-513-999C-21893	Sequence 21893, A
c 5	13	100.0	335	3	US-09-513-999C-22256	Sequence 22256, A
c 6	13	100.0	601	3	US-09-949-016-17822	Sequence 17822, A
7	13	100.0	601	3	US-09-949-016-60845	Sequence 60845, A
c 8	13	100.0	601	3	US-09-949-016-109582	Sequence 109582,
c 9	13	100.0	601	3	US-09-949-016-152975	Sequence 152975,
10	13	100.0	1617	3	US-09-248-796A-6739	Sequence 6739, Ap
11	13	100.0	2739	3	US-09-134-001C-156	Sequence 156, App
12	13	100.0	4244	3	US-09-919-039-176	Sequence 176, App
13	13	100.0	6490	3	US-09-949-016-12342	Sequence 12342, A
14	13	100.0	6491	3	US-09-949-016-15320	Sequence 15320, A

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c	15	13	100.0	11890	3	US-09-949-016-13794	Sequence 13794, A
	16	13	100.0	26173	3	US-09-453-702B-69	Sequence 69, Appl
	17	13	100.0	26173	3	US-10-114-170-69	Sequence 69, Appl
c	18	13	100.0	32039	3	US-09-949-016-16647	Sequence 16647, A
c	19	13	100.0	32043	3	US-09-949-016-12028	Sequence 12028, A
c	20	13	100.0	36028	3	US-09-949-016-14761	Sequence 14761, A
c	21	13	100.0	36755	3	US-09-949-016-16994	Sequence 16994, A
c	22	13	100.0	38059	3	US-09-328-925-4	Sequence 4, Appli
c	23	13	100.0	39433	3	US-09-949-016-12014	Sequence 12014, A
	24	13	100.0	41708	3	US-09-470-512A-3	Sequence 3, Appli
	25	13	100.0	41708	3	US-09-676-519-18	Sequence 18, Appl
	26	13	100.0	54531	3	US-09-949-016-16267	Sequence 16267, A
	27	13	100.0	60110	3	US-09-949-016-17338	Sequence 17338, A
	28	13	100.0	60110	3	US-09-949-016-17339	Sequence 17339, A
	29	13	100.0	61083	3	US-09-949-016-14144	Sequence 14144, A
	30	13	100.0	61083	3	US-09-949-016-14145	Sequence 14145, A
	31	13	100.0	64190	3	US-09-949-016-14712	Sequence 14712, A
	32	13	100.0	64190	3	US-09-949-016-14713	Sequence 14713, A
	33	13	100.0	70947	3	US-09-949-016-15165	Sequence 15165, A
c	34	13	100.0	75394	3	US-09-949-016-11754	Sequence 11754, A
	35	13	100.0	107458	3	US-09-949-016-15687	Sequence 15687, A
c	36	13	100.0	117410	3	US-09-949-016-12262	Sequence 12262, A
c	37	13	100.0	123463	3	US-09-949-016-17078	Sequence 17078, A
c	38	13	100.0	140925	3	US-09-949-016-11777	Sequence 11777, A
c	39	13	100.0	140982	3	US-09-949-016-16295	Sequence 16295, A
c	40	13	100.0	152524	3	US-09-949-016-12683	Sequence 12683, A
c	41	13	100.0	152524	3	US-09-949-016-13194	Sequence 13194, A
c	42	13	100.0	166698	3	US-09-949-016-16038	Sequence 16038, A
	43	13	100.0	256171	3	US-09-949-016-12822	Sequence 12822, A
	44	13	100.0	256176	3	US-09-949-016-15524	Sequence 15524, A
	45	13	100.0	276237	3	US-09-949-016-17504	Sequence 17504, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:05:38 ; Search time 192.696 Seconds
(without alignments)
557.883 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	13	7	US-10-662-003-8	Sequence 8, Appli
2	13	100.0	13	7	US-10-662-003-12	Sequence 12, Appl
3	13	100.0	25	7	US-10-719-956-332547	Sequence 332547,
c 4	13	100.0	185	8	US-10-674-124A-668	Sequence 668, App
c 5	13	100.0	200	8	US-10-674-124A-830	Sequence 830, App
6	13	100.0	201	8	US-10-719-993-44196	Sequence 44196, A
7	13	100.0	201	8	US-10-719-993-49906	Sequence 49906, A
8	13	100.0	339	4	US-09-925-065A-502367	Sequence 502367,
9	13	100.0	339	4	US-09-925-065A-502368	Sequence 502368,
10	13	100.0	342	3	US-09-974-300-5486	Sequence 5486, Ap
c 11	13	100.0	358	4	US-09-925-065A-138421	Sequence 138421,
12	13	100.0	360	8	US-10-727-664-16	Sequence 16, Appl
c 13	13	100.0	364	4	US-09-925-065A-565486	Sequence 565486,

					Untitled	
	14	13	100.0	367	4	US-09-925-065A-806575
	15	13	100.0	372	5	US-10-027-632-56354
C	16	13	100.0	372	5	US-10-027-632-274543
C	17	13	100.0	372	5	US-10-027-632-274544
	18	13	100.0	372	5	US-10-027-632-299463
	19	13	100.0	372	6	US-10-027-632-56354
C	20	13	100.0	372	6	US-10-027-632-274543
C	21	13	100.0	372	6	US-10-027-632-274544
	22	13	100.0	372	6	US-10-027-632-299463
	23	13	100.0	376	3	US-09-732-627A-1602
C	24	13	100.0	416	5	US-10-027-632-291518
C	25	13	100.0	416	5	US-10-027-632-291519
C	26	13	100.0	416	6	US-10-027-632-291518
C	27	13	100.0	416	6	US-10-027-632-291519
	28	13	100.0	417	3	US-09-989-890-159
	29	13	100.0	453	7	US-10-424-599-133934
	30	13	100.0	456	3	US-09-918-995-9808
C	31	13	100.0	465	8	US-10-674-124A-2131
C	32	13	100.0	474	8	US-10-357-930-51040
C	33	13	100.0	481	3	US-09-918-995-37272
C	34	13	100.0	484	4	US-09-925-065A-302871
	35	13	100.0	485	4	US-09-925-065A-502369
	36	13	100.0	492	4	US-09-925-065A-658167
	37	13	100.0	492	4	US-09-925-065A-658168
	38	13	100.0	493	4	US-09-925-065A-448418
	39	13	100.0	493	4	US-09-925-065A-728664
C	40	13	100.0	496	4	US-09-925-065A-659188
C	41	13	100.0	507	7	US-10-424-599-34243
C	42	13	100.0	511	4	US-09-925-065A-198838
C	43	13	100.0	516	5	US-10-027-632-283293
C	44	13	100.0	516	6	US-10-027-632-283293
	45	13	100.0	516	7	US-10-437-963-75673

Sequence	806575,
Sequence	56354, A
Sequence	274543,
Sequence	274544,
Sequence	299463,
Sequence	56354, A
Sequence	274543,
Sequence	274544,
Sequence	299463,
Sequence	1602, Ap
Sequence	291518,
Sequence	291519,
Sequence	291518,
Sequence	291519,
Sequence	159, App
Sequence	133934,
Sequence	9808, Ap
Sequence	2131, Ap
Sequence	51040, A
Sequence	37272, A
Sequence	302871,
Sequence	502369,
Sequence	658167,
Sequence	658168,
Sequence	448418,
Sequence	728664,
Sequence	659188,
Sequence	34243, A
Sequence	198838,
Sequence	283293,
Sequence	283293,
Sequence	75673, A

Untitled

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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 17:15:55 ; Search time 78 Seconds
(without alignments)
87.371 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4172979 seqs, 262114271 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	100.0	600	6	US-10-750-185-819	Sequence 819, App
2	13	100.0	723	6	US-10-750-185-28682	Sequence 28682, A
c 3	13	100.0	1034	6	US-10-750-185-56502	Sequence 56502, A
4	13	100.0	1300	7	US-11-112-908-255	Sequence 255, App
c 5	13	100.0	1408	6	US-10-750-185-29501	Sequence 29501, A
c 6	13	100.0	1486	6	US-10-750-185-64765	Sequence 64765, A
7	13	100.0	1709	6	US-10-750-185-38811	Sequence 38811, A
c 8	13	100.0	1905	6	US-10-750-185-46767	Sequence 46767, A
9	13	100.0	2670	6	US-10-750-185-30821	Sequence 30821, A
10	13	100.0	2696	6	US-10-689-742-35	Sequence 35, Appl
11	13	100.0	150437	7	US-11-112-908-44	Sequence 44, Appl
12	13	100.0	150491	7	US-11-112-908-46	Sequence 46, Appl
c 13	13	100.0	165627	7	US-11-121-086-89	Sequence 89, Appl

Untitled									
c	14	13	100.0	195235	6	US-10-995-561-13495	Sequence	13495,	A
c	15	12	92.3	19	8	US-11-101-244-5054	Sequence	5054,	Ap
	16	12	92.3	19	8	US-11-101-244-869445	Sequence	869445,	
c	17	12	92.3	19	8	US-11-101-244-932031	Sequence	932031,	
c	18	12	92.3	19	9	US-11-083-784-5054	Sequence	5054,	Ap
	19	12	92.3	19	9	US-11-083-784-869445	Sequence	869445,	
c	20	12	92.3	19	9	US-11-083-784-932031	Sequence	932031,	
c	21	12	92.3	25	7	US-11-121-849-131725	Sequence	131725,	
c	22	12	92.3	25	7	US-11-121-849-144373	Sequence	144373,	
	23	12	92.3	25	7	US-11-121-849-288292	Sequence	288292,	
c	24	12	92.3	25	7	US-11-121-849-295839	Sequence	295839,	
	25	12	92.3	25	7	US-11-121-849-634668	Sequence	634668,	
c	26	12	92.3	33	6	US-10-512-214-50	Sequence	50,	Appl
	27	12	92.3	201	6	US-10-995-561-19047	Sequence	19047,	A
	28	12	92.3	201	6	US-10-995-561-33092	Sequence	33092,	A
c	29	12	92.3	201	6	US-10-995-561-33636	Sequence	33636,	A
c	30	12	92.3	201	6	US-10-995-561-33765	Sequence	33765,	A
	31	12	92.3	201	6	US-10-995-561-75628	Sequence	75628,	A
	32	12	92.3	201	6	US-10-995-561-75637	Sequence	75637,	A
	33	12	92.3	502	6	US-10-750-185-2416	Sequence	2416,	Ap
c	34	12	92.3	600	6	US-10-750-185-348	Sequence	348,	App
	35	12	92.3	600	6	US-10-750-185-21724	Sequence	21724,	A
	36	12	92.3	690	6	US-10-793-626-61	Sequence	61,	Appl
c	37	12	92.3	693	6	US-10-750-185-28399	Sequence	28399,	A
	38	12	92.3	715	6	US-10-750-185-49335	Sequence	49335,	A
c	39	12	92.3	719	6	US-10-750-185-38800	Sequence	38800,	A
c	40	12	92.3	746	6	US-10-750-185-56134	Sequence	56134,	A
c	41	12	92.3	776	6	US-10-750-185-56414	Sequence	56414,	A
	42	12	92.3	788	6	US-10-750-185-48071	Sequence	48071,	A
c	43	12	92.3	810	6	US-10-750-185-54675	Sequence	54675,	A
	44	12	92.3	836	7	US-11-000-463-150	Sequence	150,	App
	45	12	92.3	882	6	US-10-750-185-60088	Sequence	60088,	A

Untitled

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 3, 2006, 16:29:54 ; Search time 888.772 Seconds
(without alignments)
684.351 Million cell updates/sec

Title: US-10-662-003-12
Perfect score: 13
Sequence: 1 GAGAATATGAATT 13

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	46	1	AU256186	AU256186 AU256186
c 2	13	100.0	105	5	C95805	C95805 C95805 Marc
3	13	100.0	119	7	CK552454	CK552454 rswla0_00
4	13	100.0	121	7	CK530459	CK530459 rswga0_00
5	13	100.0	141	3	BJ141060	BJ141060 BJ141060
c 6	13	100.0	154	9	AQ201835	AQ201835 RPCI11-63
7	13	100.0	163	9	B40165	B40165 HS-1051-A1-
8	13	100.0	168	10	CE507982	CE507982 tigr-gss-
9	13	100.0	171	1	AM013199	AM013199 AM013199
c 10	13	100.0	175	9	BZ666448	BZ666448 SGT6098-5
11	13	100.0	183	9	AQ534821	AQ534821 RPCI-11-3
c 12	13	100.0	187	11	CR348102	CR348102 mte1-8205

				Untitled	
	13	13	100.0	198 9	BH100121
c	14	13	100.0	204 10	CL200084
c	15	13	100.0	207 6	CB304637
c	16	13	100.0	215 2	BB417036
	17	13	100.0	220 10	AG263403
c	18	13	100.0	223 1	AW119916
c	19	13	100.0	228 2	BB302417
c	20	13	100.0	230 8	R77491
c	21	13	100.0	237 1	BB073681
	22	13	100.0	238 9	AZ093225
c	23	13	100.0	238 10	CE725495
	24	13	100.0	240 1	AV184517
c	25	13	100.0	245 2	BB517255
	26	13	100.0	247 9	CE051922
c	27	13	100.0	249 10	CE754025
c	28	13	100.0	250 9	CC169067
c	29	13	100.0	252 6	CD180799
c	30	13	100.0	252 9	BZ269775
	31	13	100.0	253 10	CE601599
	32	13	100.0	254 10	CG763961
	33	13	100.0	257 10	CE695869
c	34	13	100.0	259 1	AM017337
c	35	13	100.0	259 9	AZ092434
	36	13	100.0	260 2	BE190248
	37	13	100.0	260 3	BJ215786
c	38	13	100.0	261 2	BB472468
c	39	13	100.0	261 9	AZ847263
	40	13	100.0	261 10	CW661448
c	41	13	100.0	262 9	AZ034738
c	42	13	100.0	266 8	H51169
c	43	13	100.0	266 10	CW497801
c	44	13	100.0	271 2	BB345099
c	45	13	100.0	271 3	BQ310016
					BH100121 RPCI-24-2
					CL200084 ZMMBBc022
					CB304637 FLAVED000
					BB417036 BB417036
					AG263403 Lotus cor
					AW119916 sd54e07.y
					BB302417 BB302417
					R77491 yi79d05.s1
					BB073681 BB073681
					AZ093225 RPCI-23-4
					CE725495 tigr-gss-
					AV184517 AV184517
					BB517255 BB517255
					CE051922 tigr-gss-
					CE754025 tigr-gss-
					CC169067 ij88e08.g
					CD180799 MS1-0027T
					BZ269775 CH230-316
					CE601599 tigr-gss-
					CG763961 ZMMBBc020
					CE695869 tigr-gss-
					AM017337 AM017337
					AZ092434 RPCI-23-4
					BE190248 so09e10.y
					BJ215786 BJ215786
					BB472468 BB472468
					AZ847263 2M0147G17
					CW661448 OG_BB001
					AZ034738 RPCI-23-2
					H51169 yo32g01.r1
					CW497801 fsbb001f2
					BB345099 BB345099
					BQ310016 RC1-BT081



Drafts

IS&R: ("6103466").PN.

Pending

Active

Failed

("6103466").PN.

s8 and polymerase

S7 and kit

"6103466".PN. and polymerase

Saved

S1: (49) (variant mutant mutation deletion insertion) near5 myostatin

S2: (4) ("5994618") or ("582733").PN.

S3: (4) wo adj1 "9421681"

S4: (2) ("6673534").PN.

S5: (2) ("5952467").PN.

S6: (2) ("6103466").PN.

S7: (2) ("6103466").PN.

S8: (2) S7 and kit

Favorites

Tagged (3)

UDC

Queue

Trash